



1 CCATTCCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
51 GAACAGAGTG TTCTGAACAT CAACACAAAG TGGAAGAACC TTAAGCTGAA
101 GGTACAGTAT ATTATTACA CTGAAGGGGC TTGTGTGTGG ACAAGAAAGC
151 GCTGACAGCT CAAATGGATC CCATGGAAC TGAAGAAATGTC AACATCGAAC
201 CAGATGATGA GAGCAGCAGT GGAGAAAGTG CTCCAGATAG CTACATCAGG
251 ATAGGAAATT CAGAAAAGGC AGCAATGAGC AGTCAATTTG CTAATGAAGA
301 CACTGAAAGT CAGAAATTCC TGACAAATGG ATTTTGGGG AAAAAGAAGC
351 TGGCAGATTA TGCTGATGAA CACCATCCCG GAACCACTTC CTTTGAATG
401 TCTTCATTTA ACCTGAGTAA TGCCATCATG GGCAGTGGGA TCCTGGGCTT
451 GTCCTATGCC ATGGCCTACA CAGGGGTCAT ACTTTTATA ATCATGCTGC
501 TTGCTGTGGC AATATTATCA CTGTATTGAG TTCACCTTTT ATTAATAACA
551 GCCAAGGAAG GAGGGTCTTT GATTTATGAA AAATTAGGAG AAAAGGCATT
601 TGGATGGCCG GGAAAAATTG GAGCTTTTGT TTCCATTACA ATGCAGAACA
651 TTGGAGCAAT GTCAAGCTAC CTCTTTATCA TTAAATATGA ACTACCTGAA
701 GTAATCAGAG CATTGATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
751 CAATGGCAAC TACCTCATCA TATTTGTGTC TGTGGAATT ATTCTTCCAC
801 TTTGCTCCT TAAAAATTTA GGTATCTTG GCTATACCAG TGGATTTTCT
851 CTTACCTGCA TGGTGTTTT TGTTAGTGTG GTGATTTACA AGAAATTCCA
901 AATACCCTGC CCTCTACCTG TTTTGGATCA CAGTGTGGA AATCTGTCAT
951 TCAACAACAC GCTTCCAATG CATGTGGTAA TGTTACCCAA CAACTCTGAG
1001 AGTTCTGATG TGAACCTCAT GATGGATTAC ACCCACCACA ATCCTGCAGG
1051 GCTGGATGAG AACCAGGCCA AGGGCTCTCT TCATGACAGT GGAGTAGAAT
1101 ATGAAGCTCA TAGTGATGAC AAGTGTGAAC CCAAATACTT TGTATTCAAC
1151 TCCCGGACGG CCTATGCAAT TCCTATCCTA GTATTTGCTT TTGTATGCCA
1201 CCCTGAGGTC CTTCCCATCT ACAGTGAAC TAAAGATCGG TCCCGGAGAA
1251 AAATGCAAAC GGTGTCAAAT ATTTCCATCA CGGGGATGCT TGTGATGTAC
1301 CTGCTTGCCG CCCTCTTTGG TTACCTAACC TTCTATGGAG AAGTTGAAGA
1351 TGAATTACTT CATGCCTACA GCAAAGTGTA TACATTAGAC ATCCCTCTTC
1401 TCATGGTTG CCTGGCAGTC CTTGTGGCAG TAACACAAAC TGTGCCATT
1451 GTCCTCTTCC CAATTCGTAC ATCAGTGATC AACTGTTAT TTCCCAAACG
1501 ACCCTTCAGC TGGATACGAC ATTTCTGAT TGCAGCTGTG CTTATTGCAC
1551 TTAATAATGT TCTGGTCATC CTTGTGCCAA CTATAAAATA CATCTTCGGA
1601 TTCATAGGGG CTTCTTCTGC CACTATGCTG ATTTTATTTC TTCCAGCAGT
1651 TTTTATCTT AAACCTGTCA AGAAAGAAAC TTTTAGGTCA CCCCCAAAGG
1701 TCGGGGCTTT AATTTTCTT GTGGTTGGAA TATCTTCAT GATTGGAAGC
1751 ATGGCACTCA TTATAATTGA CTGGATTTAT GATCCTCCAA ATTCCAAGCA
1801 TCACTAACAC AAGGAAAAAT AC (SEQ ID NO:1)

FEATURES:

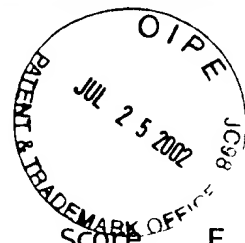
5'UTR: 1-163
Start Codon: 164
Stop Codon: 1805
3'UTR: 1808

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FIGURE 1A



HOMOLOGOUS PROTEINS:

Top BLAST Hits:

			Score	E
CRA 145000039337444	/altid=gi 12017941	/def=gb AAG45335.1 AF295...	975	0.0
CRA 114000033649823	/altid=gi 10945621	/def=gb AAG24618.1 AF298...	597	e-169
CRA 160000003782430	/altid=gi 8677401	/def=gb AAF75589.2 AF1736...	591	e-168
CRA 148000002720069	/altid=gi 8248427	/def=gb AAF74195.1 AF2496...	587	e-166
CRA 87000000006802	/altid=gi 7243145	/def=dbj BAA92620.1 (AB03...	578	e-164
CRA 18000005069115	/altid=gi 5870893	/def=ref NP_006832.1 tran...	500	e-140
CRA 88000001154721	/altid=gi 7406950	/def=gb AAF61849.1 AF15985...	496	e-139
CRA 66000019404613	/altid=gi 9506837	/def=ref NP_061849.1 amin...	495	e-139
CRA 100000004435450	/altid=gi 8926332	/def=gb AAF81797.1 AF2730...	492	e-138
CRA 335001098689635	/altid=gi 11434147	/def=ref XP_006635.1 hy...	480	e-134

EST:

gi 10934204	/dataset=dbest /taxon=96...	1072	0.0
gi 10286121	/dataset=dbest /taxon=96...	718	0.0
gi 9872634	/dataset=dbest /taxon=960...	680	0.0
gi 2656674	/dataset=dbest /taxon=9606 ...	549	e-154
gi 9882497	/dataset=dbest /taxon=960...	541	e-151
gi 689641	/dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10934204 whole embryo (mainly head)
 gi|10286121 Hepatocellular carcinoma
 gi|9872634 Non-cancerous liver
 gi|2656674 Fetal liver spleen
 gi|9882497 Non cancerous liver
 gi|689641 Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

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FIGURE 1B

Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



1 MDPMELRNVN IEPDDESSG ESAPDSYIRI GNSEKAAMSS QFANEDTESQ
51 KFLTNGFLGK KKLADYADEH HPGTTSFGMS SFNLSNAIMG SGILGLSYAM
101 AYTGVILFII MLLAVAILSL YSVHLLKTA KEGGSLIYEK LGEKAFGWPG
151 KIGAFVSITM QNIGAMSSYL FIIKYELPEV IRAFMGLEEN TGEWYLNNGY
201 LIIFVSVGII LPLSLLKNLG YLGYTSGFSL TCMVFFVSVV IYKKFQIPCP
251 LPVLDHSVGN LSFNNTLPMH VMPLPNNSSES SDVNFMDYT HRNPAGLDEN
301 QAKGSLHDSG VEYEAHSDDK CEPKYFVFNS RTAYAIPILV FAFVCHPEVL
351 PIYSELKDRS RRRKMQTVSNI SITGMLVMYL LAALFGYLT F YGEVEDELLH
401 AYSKVYTLDI PLLMVRLAVL VAVTQTVPIV LFPRTSVIT LLFPRKPFWS
451 IRHFLIAAVL IALNNVLVIL VPTIKYIFGF IGASSATMLI FILPAVFYLK
501 LVKKETFRSP QKVGALIFLV VGIFFMIGSM ALIIDIWIYD PPNSKHH (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 5

- 1 83-86 NLSN
- 2 260-263 NLSF
- 3 264-267 NNTL
- 4 276-279 NNSE
- 5 369-372 NISI

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

503-506 KKET

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 7

- 1 33-35 SEK
- 2 49-51 SQK
- 3 129-131 TAK
- 4 290-292 THR
- 5 360-362 SRR
- 6 473-475 TIK
- 7 506-508 TFR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 5

- 1 18-21 SSGE
- 2 22-25 SAPD
- 3 129-132 TAKE
- 4 305-308 SLHD
- 5 309-312 SGVE

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FIGURE 2A



[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 6

1	95-100	GLSYAM
2	153-158	GAFVSI
3	164-169	GAMSSY
4	186-191	GLEENT
5	296-301	GLDENQ
6	482-487	GASSAT

[6] PDOC00009 PS00009 AMIDATION
Amidation site

58-61 LGKK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

FIGURE 2B

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BLAST Alignment to Top Hit:

>CRA|145000039337444 /altid=gi|12017941
/def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
transport system A3 [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=547
Length = 547

Score = 975 bits (2492), Expect = 0.0
Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1 MDPMELRNVNIEPDDDESSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
MDP+ELR+VNIEP ++S S +S Y +GNSEK AM SQFANED ESQKFLTNGFLGK
Sbjct: 1 MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGAMDSQFANEDAESQKFLTNGFLGK 60

Query: 61 KKLADYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMAYTGVLFIIMLLAVAILSL 120
K L DYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61 KTLTDYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121 YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAFVSITM QNIGAMSSYLFIKYELPEV 180
YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAF+SITM QNIGAMSSYLFIKYELPEV
Sbjct: 121 YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAFISITM QNIGAMSSYLFIKYELPEV 180

Query: 181 IRAFMGLEENTGEWYLN GNLYIIFVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW 240
IR FMGLEENTGEWYLN GNLY++FVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW
Sbjct: 181 IRVFMGLEENTGEWYLN GNLYLVFVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW 240

Query: 241 IYKKFQIPCPPLVLDHSGVGNLSFNNTLPMHVMLPNNSESSDVNFMDYTHRNPAGLDEN 300
IYKKFQIPCPPLVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHR+P GLDE
Sbjct: 241 IYKKFQIPCPPLVLDHNNGNLTFNNTLPMHVIMLPNNSESTGMNFMVDYTHRDPEGLDEK 300

Query: 301 QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPIILVFAFVCHPEVLPIYSELKDERS 360
A G LH SGVEYEAHS DKC+PKYFVFNSTAYAIPIIL FAFVCHPEVLPIYSELKDERS
Sbjct: 301 PAAGPLHGSGVEYEAHSGDKCQPKYFVFNSTAYAIPIILAFVCHPEVLPIYSELKDERS 360

Query: 361 RRKMQTVSNISITGMLV MYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLL MRLAVL 420
RRKMQTVSNISITGMLV MYLLAALFGYL+FYGEVEDELLHAYSKVYT D LLMRLAVL
Sbjct: 361 RRKMQTVSNISITGMLV MYLLAALFGYLSFYGEVEDELLHAYSKVYTFDTALL MRLAVL 420

Query: 421 VAVTQTVPIVLFPIRTSVITLLFPKRPF SWIRHFLIAAVLIA LNNVLVILVPTIKYIFGF 480
VAVT TVPIVLFPIRTSVITLLFP+RPFSW++HF IAA++IALNNVLVILVPTIKYIFGF
Sbjct: 421 VAVTLTVPIVLFPIRTSVITLLFPRRPF SWKHFGIAAIIIALNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFY LKLVKKE TRSPQKVGALIFLVVGIFFMIGSMALIIIDWIYD 540
IGASSATMLIFILPA FYLKLVKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481 IGASSATMLIFILPAAFY LKLVKKEPLRSPQKIGALVFLVTGIIFMIGSMALIIIDWIYN 540

Query: 541 PPN SKHH 547
PPN HH
Sbjct: 541 PPNPDHH 547 (SEQ ID NO :4)

>CRA|114000033649823 /altid=gi|10945621
/def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
transporter system A [Homo sapiens] /org=Homo sapiens

FIGURE 2C

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/taxon=9606 /dataset=nraa /length=506
Length = 506



Score = 597 bits (1522), Expect = e-169
Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1 MDPMELRNVNIEPDDESSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57
M E+ +I PD++SSS S D SY +++AA+ S +A+ D E+Q FL
Sbjct: 1 MKKAEMGRFSISPDEDSSSYSSNSDFNYSY-----PTKQAALKSHYADVDPENQNFLLSN 56

Query: 58 LGKKKLADYADEHHPGTTSTFGMSSFNLNAIMGSGILGLSYAMAYTGVLFIIMLLAVAI 117
LGKKK Y E HPGTTSTFGMS FNLSNAI+GSGILGLSYAMA TG+ LFII+L V+I
Sbjct: 57 LGKKK---YETEFHPGTTSTFGMSVFNLSNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

Query: 118 LSLYSVHLLLKTAKEGGSLLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYEL 177
SLYSVHLLLKTA EGGSL+YE+LG KAFG GK+ A SITMQNIGAMSSYLF+KYEL
Sbjct: 114 FSLYSVHLLLKTANEGGSLLYEQLGYKAFGLVGKLAASGSITMQNIGAMSSYLFIVKYEL 173

Query: 178 PEVIRAFMGLEENTGEWYLNNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTOMVFFV 237
P VI+A +E+ TG WYLNNGNYL++ VS+ +ILPLSL +NLGYLGYTSG SL OMVFF+
Sbjct: 174 PLVIQALTNIEDKTGLWYLNNGNYLVLLVSLVILPLSLFRNLGYLGYTSGLSLLOMVFLL 233

Query: 238 SVWIYKKFQIPCPPLVLDHSVGNLSFNNTLPMHVMPLPNSESSDVNFMDYTHRNPAGL 297
VVI KKFQ+PCP+ + N + N TL ++P
Sbjct: 234 IIVICKKFQVPCPVEAA--LIINETINTLTQTALVP----- 269

Query: 298 DENQAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELK 357
+ + +D C P YF+FNS+T YA+PIL+F+VCHP VLPIY ELK
Sbjct: 270 -----ALSHNVTENDSCRPHYFIFNSQTVYAVPILIFSVCHPAVLPIYEELK 317

Query: 358 DRSRRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRL 417
DRSRR+M VS IS M +MYLLAALFGYLTFY VE ELLH YS + DI LL+VRL
Sbjct: 318 DRSRRRMNVSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLIVRL 377

Query: 418 AVLVAVTQTVPIVLFPRTSVITLLFPKRPFSWIRHFLIAAVLIAALNNVLVILVPTIKYI 477
AVL+AVT TVP+V+FPIR+SV LL + FSW RH LI ++A N+LVI VPTI+ I
Sbjct: 378 AVLMAVTLTVPWIFPIRSSVTHLLCASKDFSWRHSILITVSILAFTNLLVIFVPTIRDI 437

Query: 478 FGFIGASSATMLIFILPAVFYKLKVKKETFRSPQKVGALIFLVGIFFMIGSMALI IIDW 537
FGFIGAS+A+MLIFILP+ FY+KLVKKE +S QK+GAL FL+ G+ M GSMALI++DW
Sbjct: 438 FGFIGASAASMLIFILPSAFYIKLVKKEPKSVQKIGALFFLLSGVLVMTGSMALIVLDW 497

Query: 538 IYDPPNSKH 546
+++ P H
Sbjct: 498 VHNAPGGGH 506 (SEQ ID NO :5)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00398	1/1	90	110 ..	1	23 [.	4.0	4.8

FIGURE 2D

Docket No.: CL001010
Serial No.: 09/776,705
Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

PF01490	1/2	99	236 ..	1	179 [.	58.9	2.5e-14
PF01490	2/2	305	529 ..	200	467 .]	133.9	3e-36



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FIGURE 2E



1 AGCTTAGCAA TATGGATCAA GAGGTCCAAT ACCTGATTAA TAAAAGTTTC
51 AGGAGTAAAC AAAGGGGAAG AAATAGTTTT TTAAATAGT AGAACTTTTT
101 TTATTTTGTAG AAAATGTGTC TTCTATAGAA GAAAGACAAG CCTTTTGATT
151 GGGCCGCTCTG CATGCTGAGT ATGATGAATT TAAAAAGCGA CTCACATCTA
201 GTCACGTCGT GATGAAAGGA TAAGGATAAA AATTCTGAAA TCCTCAGAAA
251 ACCATCGATA AATTATCTAT AAAGAAATAA GAGCCAGACT CATCAATAGA
301 AGCTAGAAGA GAGAAGTTTC TTCAATATTC TGAAGGAAAA TGCTTCTGAA
351 TCTAGAATTC AAACAATTAA CAAAGTTTGA AGGCAAAATA AAGAATTTTC
401 CAACATGAAG CAACTCAGAA ATTCTATTTA CAGACATAGG CTCATTGTGT
451 GAAAAAGTT ATTCAAGGCA TTATTTTAGC ATAATGCAAA ATAAACTGAA
501 GAAAGAAGAT AGAATGCCGT TCAAGAACT AGCAGCTGAG CAAGACTCAG
551 AGGTTGGAGG AGGAAGCCAT TCAGAATGAG AAAGAGCATA GAAAATTTGC
601 TTTCAAAGTT TTGGTAATAT AGAATTATAT TTCACTTATT ATGTAGTCAA
651 ATACACCACT TTGTCTTTAG GGCATACTAT TTATACAGTG ATAATACTGT
701 AATTGCTGCT TATTGGTTTT CCATGTTTAG AAACAACCTA CAGGCAAGTT
751 ATGACACTTG TTTACAGAA CAAGATGAAA ATATTATGAT TCTCAAATTG
801 TAAAAGTATT TTATTAATA AAATAATTAG GAGTGTAGGA GAAGGAAGGA
851 AAGAAAGAAA AAGTATGCTA ATGTCCTTAT TTTTATGGG TAACCAGTCT
901 AAAATCAGTA AACCAAGTCA AAAAAGCTTT AGTGAATTAT TCAGATCTAG
951 AATGGCTAAC TTTAAGTAAC AAGCTAAAA CAGAAACCGT CAATAGTGGT
1001 TGCTGCTGGG AAGTGAGACT GGTACTGTGT GAAGAATGAG GAAAACCTTT
1051 GTAATCATTT AGTGAGTTTC TTTTTTTTTT CTTTACCCA TATGCATGTC
1101 TTACTTCTAT TCTCTCTTAG CTTTAACTT GCTTCTTTTC ATCTTTTATG
1151 TATATACATT TAGGCTGCCT TATATTAATA ATAGTTTCAT TTTTGTTCCT
1201 CCTGCTTAAA ACACTGTGTG CTATTTTTTT AAATTCTGAG AACTGCTTTC
1251 TTTATTTCTA GACAATTCTC TGCCATTATC TCTTCTGTT TTGTCTCACC
1301 CTAGTCTCAC AATTCTCTAT ATTGGAATGA CTATCAGTGT ATATTTGAAC
1351 TTGTAATTCT TATTTTTTCC CCATTCCTCT TAACCTCTTA TTTGTATTTT
1401 TCTTTTTTTA ATCTCTTCAT GCTATAATTT GAGTGATTTT CACAGATCTG
1451 TCTTTCAATT TTATAAGTCT TCCTTCAGCT GAGTTTTTTT AAATTTCAAT
1501 GATTCTATTT TTTTCTTTTT TTTAAGAATT CCTTTTTTTG ACTCTTTTTG
1551 CAACAGCCTG TTCTCCTTTT ATATTCCTTT ATAATGTTTT TATTCTGTGA
1601 AAGTTATTCT CTTATTTTGA ATGTTTTCTT TCAAAATGTC TTTCTTTTTA
1651 TTAATTTAAT GTAAAAGTCC CTTTTAAATT GCTTTGTTAT TTGTAGTTCC
1701 TTAGATGTGA ATTTTATCAT TTCTGTGACC TACTGGCACT CTTGCTAGTG
1751 AGTTTCCATG TGTGTTCTAT ATGTTTTGTA ATTTGAGGAT GTGAACTTTT
1801 CTCAAGTGTG AGTTGCCTTT CAAAAAGTA CTGCCATGGC ACTGGGTTGT
1851 GGAGGTATTC CCATGTGGTA GTTCTGTTT GTCAGAGGAA TAGCACATTT
1901 TGTGACTTCT GGAGCAATTT TTATGTTAGT TTCTCTGCTC AAGATTTTCT
1951 TATCAAATGG GTATTGCACA TGTCATGACC ACATTTTCA AGAATGATAG
2001 TGTTTCTCCT AATACGATGG TTCAACAATA ATTGAATGAA TCTAATGGTA
2051 AGAATTTTCA AAGAAATTAT ATCAACTACA TATAGTAGAT TCAAGGCATT
2101 TTTCAAAAAC ACAATGCCAG TCCACCCCTT TCACTATAC AATTGAGGAA
2151 AATGAGGTCC CCAAATGTTA AATGACTTCT GCTGAGATCC AATGAATTAA
2201 AGGCAGAGCA GAGGCTAAAA TCTAGATCTC TTTGTTGTTA AAATACATTT
2251 TAATTTGACA CAGATGATGA GTAATGCTGA CCCAGAGGTA AATCTGAACT
2301 TTCTTTTGT ACTATTCTTA ACTTTGGCTT CAGGATCCAA GTGCCTAGAA
2351 AGTTACTTCC TAAACTTGAT CCTCACCTAT GTTGCATATT ATCAAGCATT
2401 TGGTGGTGT AATTCTTTCA TGTCCAATTA AATTAAGCA GTAATTTTCT
2451 TTCTAGTTAT TGCTAGTAGA GAACTGGTA GATTCTGCCT TGGTAGACCT
2501 TCCTCTGTCA ACAATTTACT TTTGTCTTCC TTTCTTTTAA AACATGTATC
2551 CCACCTCAAA ATACCTAAAT TTCCTTGAAG ACTGCTGCCA TGTTTTAAGA
2601 TTTCTTTTTT TTTCCATAGT GACTAGTAAA ACCTGCCATT TTCATTATAC
2651 ATAGGCACTC TATAAATATC TGCTAATTTA GCAATTATTA GTAATTTTCT

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FIGURE 3A



2701 TTCTTCTCTT CCATTTCTTC CTTTCTTGTA TTGGGTAAAG GAACATTTCA
2751 GGATTTGCTT ATGTAAAGTT TTCAGGAGTT TCTTTCCTTC CTCCCTTTTA
2801 CAGAGAGCAT ACAAAATGTA GATGATTCAT ATTCACATTAT TTCATTTAAA
2851 TAAAATTATA ATGATGTATG TTGTGTTCTG TTTGCAGAAC AGAGTGTCTT
2901 GAACATCAAC ACAAAGTGGA AGAACCTTAA GCTGAAGGTA CAGTATATTA
2951 TTTACTCTGA AGGGGCTTGT GTGTGGACAA GAAAGCGCTG ACAGCTCAAA
3001 TGGATCCCAT GGAAGTGAAG AATGTCAACA TCGAACCAGA TGATGAGAGC
3051 AGCAGTGGAG AAAGTGCTCC AGATAGCTAC ATCGGGATAG GAAATTCAGA
3101 AAAGGCAGCA ATGAGCAGGT ATGGGGTTAA AAATTACTAT GTTCCATGGA
3151 AAAATAAGAC AGGATGTGGA CATGGAAAAC AGGGTCTTGA TGGGAAGAAC
3201 TGGATTTATT ACAGGTAAAT TTGTGATAAC AATGATATTG ATGCTAGCAC
3251 ATCAATTCCC TGGTCTGAA ATACAGTGAT AATGTCAATC TCTTTTGTGA
3301 CTGATTTAGA ATTGAGGTTA CAATGTCTTT GTCTCCATTA ATAATGTGTA
3351 ATAATTTTAA TTATTTTAGC CTATTGCTCC TCTTATCTTT CTCAGATTCC
3401 TCTTTGAATG TTGCTACACC TCCTGGTTTC TGTAGGGATT CTTTTCTCTC
3451 TAAAAGTATC CTCTGGGCAA GCTCACTCAC AACTACTATG GCCTCACCTT
3501 CCAAATATAT GCCATATACC CAGCCTGTTA AGTTTCTCTA CTGAATTTCA
3551 GATAATTATA TCTGAATGTC TACTGCACGT CTCTACTGGA CCATTACTGT
3601 GTCTAAATTG CCTCATTTAT AAAGTTAAAC CTGTAATGTC TAATACTGAA
3651 CTCCTATCTT TCCCTCCAAA ACCTGCTCCT CCTCTAGTAA TCCCCATCCT
3701 AGTGAAAATC ACTGCTATCA TGTAGCAACT CACTCAAAAG CCCCTAGGTG
3751 TAAACTTTGA CCCACATAGC CAACGGTCAG TCATATCCAG TTGGTTTGAC
3801 CTTATTAATG CTTCAAATAC ACCTACTTTT CTGTACCCAT TCTACTGTGG
3851 TCTTACGTTA GGCCTACATT AAATGTGAGA CAGGGAGAGA GCCCTGATTT
3901 CTCTCCCTGT CTTACATTTT GCTCTCCTCT GTCTAGCCCT CTACACTCCT
3951 GCAAGAGCAA TCTCTTACAA TTGCAAATTG AATCAATTTT CATCCTTAGA
4001 TAAAGCCCTT CTGCACCTCT CCAATAGCCA TAAGAGAAAG TAGATTACAC
4051 ACACTGCTGG GCACGTAAGG TCCTTTGTGA TCTGTTCTTG ACCTGCCCTT
4101 CCTGTCTGT TTTTGGCCCT CTCCCTATTT GTTACTTGTT GCCTTCACTC
4151 ATTCTGCTCC AACTGCCTGG AATCAGTCAC CTGCTCCCCC TTTCTCCGTG
4201 TTGACACCTC TCATCCTTCA AGAATCAGCT CAACATCAGG TCTCCTATGC
4251 AGCCTTTTCC AAATTACTCT ACTCCCCCAT GTAGAAGTGA CTGCCCCTCC
4301 TTCATGTACC CTCTCCCTGT GCAGATGTTA ATTACGCCAC TACTACAGGT
4351 TAATGGCCTC TGTGGTCCCA CCACCTGCCA CATTGTCTGG TGCATAGTGA
4401 GTGACAATA GTTATTTGAT AAGTCAATTG ATTTCCCACA AAATGTTATA
4451 TCAAATTGTA CATGATTTAA GATGCTCAGA AGGGAATTTT TGACCAAATC
4501 TAGGCGTGAA ATAGAGAATA TTGTGCTCAA ACAAAGACTT CTCATTTTAT
4551 TTACAACACC CAGGAAAATC CATCAGGAGA AACTACCGTT CTTCTTCAA
4601 GTAGCTCAGT GCAATGAACT TTAGGGATGT CGGACTAGAG AGGCCACTGA
4651 GATGTAAATT ATAGCATTTT CTAATTTAGG TGACCCTTGA AGAAACACTA
4701 GGGTGCTAGA AGACAGGGCT TTGGAGTCTG CAGAGTAGTT GCCTGACTTT
4751 AGAGAAGCTG TTTGTCCTCT TTGAGCTTCA ATGGAAAATG TAAAATGGCA
4801 AACCAACAGC TGCTTTTCAA GGATGAGATG GGTGACCAGA ATATAGATGA
4851 CATTCAATAC TTTTATTA CTCTCCTTC ACTGCATTAC CCTCAGTAAA
4901 TTGATTCAAA CCTGAGGATG TTTCTGAAAG GCATGCACAC AAATATGAGC
4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCCTAA GAACTGTCAT
5001 AGTGTCAATC CACTTGATCC TCAAAAGCCA GAGTAGAAAG AGCATGAATG
5051 CTTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCCTCAC AGTGACTTAC
5101 CTTTTATCTC CTGGCTTAAA CATAGGACAT CATTTTGCAG TTTTAAAAAT
5151 CAGTTTAAAG AGATGGGTTT TATCTATGTG TGGTTTGGAT TGAACCCTTA
5201 AATGTAAATT TTTGAGAAAT TCAACATAAT GTATTTATTT GTGATCATT
5251 TACTTGTGTT TTCAATACAT GCTGGGTTTG GTATCAAAAC ATTTAACATA
5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAATGACT
5351 ACAACTCATC TCATGCCAAA ATAAGAACAT GCAAATGCCT CAAAGAAAGA

FIGURE 3B

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5401 AAATCTGTTT ACTTTCAAAT TCTCAATTTT AAAAACTACT ATGGAATACA
 5451 GATTTTAGTT TATTGATTAA AATAAAGATT CCAGAGTTTA AATTCTAGGT
 5501 GGCACTTTGT TTTTATAGT CCTCAGGCCC ATTTTAGGCT TCATTTTATC
 5551 CTGTCATCTC AGTCTCCAAC TGTGAACATT ATGTACCAGT CTTACATAG
 5601 CAGGTACATT AATTACAGAC CATTAATGTA AACCACAAAA GAGTGGTGGG
 5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CTGAGGGCAT
 5701 TGTGCTTTCT GTGAGAAATA TGGGGAGAAG GCTAGGAAAT GTTCTTAACT
 5751 TGTGACTCA GAGCTATTTA TGCCTTGAGT TCTAGAAAAG CACATACAAC
 5801 TTTGTGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTTCTATT
 5851 CTCAAAAAGT AACCTGTCA TCCTCTTTCC TCTCCAGATT ATTTTCAGGA
 5901 TTAGCTTCTG TTATAAAAA TAGCTTGTA AGATCTCCTA CAATAATTAT
 5951 TTTCTATTTT ATTTCTAAGG TTTATTTATT TATTTATTGA GACAGACAGA
 6001 GTTTCACCTC TGTGGCCCAT GCTGGAGTGC AATGGTGCAA TCTCGGCTCA
 6051 CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCT TCAGCCTCCT
 6101 GAGTAGCTGG GATTACAGGC GCCTGCCACC ACACTCGGCT AACTTTTGT
 6151 ATTTCTAGTA GAGACGAAGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC
 6201 TCCTGACCTC AAGTTATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT
 6251 ACAGGCGTGA GCCACTGTGC CTGGCCTCTA GGATTATATT AATAGAACAA
 6301 TCTTCAATTA TTTTATCTTT CTTTATCTTT CTTTTCATGT AGGAAATGTC
 6351 CTAAAATTTT CAAACCCTCA ATTTGAAAGC ACTTTTAAAA TCATACATAG
 6401 TCGAGCATTT TATATAAAAA CAACTAAAAA GTCTGTGACA TTTTGCAGTA
 6451 TAAAAATGCA ATGGCAGCAG CAGGCCTTAT TAATTGAGCC TCTTGGAAAT
 6501 GTGGCTGGTC CTAGGTCCGT AGCCTCAAAG GCCCTGGCTT GTAACCTGCAG
 6551 GAGCTGACCA GCACAGCTCT ATAACCAAGT TGTACATCTT CTAGCCTGTG
 6601 TCCAAGAAAA CCAGAATCAC AACGCTCTGT GGATAGTGAC ATCTTAAAGT
 6651 TTTCTTTCCC TCCCAACTCT TTTGCCAGTT CATTGAATTG CTTTAATAAT
 6701 TTCCTTAGTT TCATTCATTA TCTGTTAATA ATCCATGTAC ATTTTGAGAG
 6751 TAATTAANAAC ACATACGCAC ACACAGAAAC AACCAACACA ACACACAGCT
 6801 ACCACTGAAT TACTTTCCAG TAAGAGATGT ATGTATAAAT GATTGTACCA
 6851 AAAAAAAAAA AAGAAAGAAA ATACCAGCTA CAGGGCCCTG CCTGGGACTG
 6901 CTTGATGCCA GGGGGAGAAT GGGGTCTCCC CCTGGGTATG GGTGGGTATG
 6951 GGCCTGCTGC TTCACCTTTC TGAGCCACAG TTCCCTATAG GGATATTTTG
 7001 AACATCAGAT GAGATAAGGA TCACAGTGCC TAGGCATTTA ATAAATATTC
 7051 GTTGAATTAA TAAAATCATC TGATTATGGT ATGGTAGTAG TTCAGAAAAT
 7101 TCTGTCATAA CCCTGTACTC TTTCTTTGGA AGGGCTCTAA ATGGGAACAC
 7151 AATTAGTTGT AGTCTCTTGC ATAGCTAATG TGAGAAAGAG GGAATGTGGT
 7201 ATAAACAATT TTTTAACTAA AAATAATATT TCCTTCCTTT ATAACATCCT
 7251 TCTTCCATCC CAAAGTATAG TTGTAATGG AACTCAAAT TGTTGGTCTG
 7301 GAATGACCGT TAGTGTGAAG GAGGAAAAGA AAATTGGGGT GTCTTATTTT
 7351 CCCTCCTCTG ATTCAGTTAC TTAGATCACC TGAAACATAC ATATGATTCA
 7401 GAGCATATAT TTAGATGTTT TCACTTTCTT ATTTGTGTGT GTGTGTGTTC
 7451 AGTCAATTTG CTAATGAAGA CACTGAAAGT CAGAAATTCC TGACAAATGG
 7501 ATTTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CACGTAAGTG
 7551 AATCTATGCT TTCAGGCAAT AAACGGGACT GAGGGTGTCT GATCTACCTA
 7601 GGTCTCTGTG GGAAAACAAT GTGACTGAAA TTTTCCAAGC CTTGATCAGC
 7651 ACATTCTGTG TTTATTGAGG CTCTTACTGG AATAAGGGCT TGTTTTTTCC
 7701 TGTTCCGCAT ATGGCTGCAT GAATCATTTA TGAACTTAT GTGTTTTGGG
 7751 GGGAAATCAT TCTAACCCAA AGGTAATCTA CAATCATACA TGTTCCTT
 7801 TCTTTATGTG ACTCCCCTTG TAATTTGTAT TTTTACTGAG GCCTCTGCTG
 7851 AAACCAAGCA CTGCATTCCG TTGAAAATTA CATGCTTTTA TTGATGTTGA
 7901 GTAATGGCTT TACTCCTGTA ATGTTATCTT AGTCTTCAAT TTTGGACTGT
 7951 AATCTGCAGA TAATGTGAGA ATAAGGATAA CCCCTAAAGG TATGCCCTTT
 8001 GGCAAATGTT TGCTTATAAT ACATCCCTTC TTTTCAAGC ATCCCGGAAC
 8051 CACTTCCTTT GGAATGTCTT CATTTAACCT GAGTAATGCC ATCATGGGCA

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FIGURE 3C



8101 GTGGGATCCT GGGCTTGTCC TATGCCATGG CCAACACAGG GATCATACTT
8151 TTTATGTAAG TGAATGTATA TGTCTACATT TGGTGATGAA GTCCATGCAT
8201 ACCTGGTGGC TTTTTC AATT AACAACTCTCA AGTTTGATCT TTGTGAACGT
8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTCACCCA ACCATCCCTA
8301 ACCCAACGGC AGAAAGTGTA TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
8351 CCTCGCCAGA AGAATTTTGT TATTCAGTAA ATACTTGAAA TAATTTGGTG
8401 TTTAGCAACC AAAAAAGATCT TTCCAGAAAG CAAATCTGAT TTTATCTCAT
8451 TCTTAGGAAA GAAGCAACCA AGCCTAAGAG CCCTGCATGC CCTTGCCTAC
8501 CTTATGTCCC ATTCCCTGTA CCCCTGTGCG ACAGATACAC TGGGCACAAT
8551 AGCCTTCTCT CCATCCTATG AAGATGCCAC ATTCCCTCTC ACCATTGGAC
8601 CTTTGACAT GGTCTTGAA CCCTCTTCTC TTCCTTCTTC ATCTAGTTAA
8651 CTCCTCATAT GTCAGTTCAG TCTCACCTGA ATACTGCGCG CCCTGATCTC
8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCACA ATTTTAATGT
8751 TTTAGTGCCA TTTGTCTGAT TCATTTGGTT AATATCTGTC CCTCTTGCTG
8801 GACTATAAGC TCTAGAAAGT TGAGCCCATG TCTGTTTTTA CTCACCAATG
8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTTGTTGA
8901 GTGACCAAAC CTTATTCTTA AACCTACGTA CTTTCACCAA ACTTGTTCAA
8951 ATGCTGCCTA AGGGTAGCAG CATCTGGTAG TTGACCTGTA GGGTGGATAC
9001 TGCAGTGTCT ATGACAGACA ACAACAGACG TTTATGTGCA TCATGTACAG
9051 CCTGGCATT TCCAGGATAT AGTTGGCAGC AGTGAATTC TTCACAAGAA
9101 TAAAGTCTGA TGTTAGGCAC CACTGTGGAC ACAGATCCTA ATCCCAAATG
9151 CAACGCTAGA GAGTTAAATA ACTGTCTAAG AATGCAACAT TTATATCACA
9201 AATATGTGCT GTTTATGTTT TGAATATCAC ATATGATTAG TAATCACACA
9251 GCTATTTGAG GGCTAAGCAT CAGGACTATA AATATTTGTA TTGTGTTAGT
9301 GCTTTGATTG AACTCTTTTA TGTATAATAT TCTTCAGCTG AATGGGTTTT
9351 TATATCAACT TTACTTTTAT ATAAGCCATG TTTTGAAATA AACTAGGATT
9401 TTAATAATCT GAATTTTAAT AGCTATGTAT GTAGTCATAT ATTTGTATGC
9451 TTTTGTAATG TGCTTACCTC TAAGACAAAA AAACCTGCCT TTCCTTATTA
9501 ATTATACATA CCATTAAAAT GAATTAGGAA GTTACAGATC ACTGATGAAT
9551 AGAAATAGGA AAAACTTCCC CCAATCCCAC AGTCATAGAT CATCTTCATG
9601 AGAGAAGAAT GTTCCACTTT TTAATAATGAG GGCCTCATT TAGGCTTATA
9651 AACACTTAGC AGATGAATTT GGTGAGAACA ATTAAATCAC TAAACATCAT
9701 GGGGTGTGTT TTGTGTGTCT AAGTAGCCCA GACTGGATTA AGCTTTCTCT
9751 CTTAATTTAT AGCAAGTGAC ACAGTATTTT AAAGGTTTTA CTCTTAGTAT
9801 TTTCTGCCAG AGAAAGTACA TGTTTAGAAT ACAGGGAATG CTCATTATTT
9851 TTCCAGGGAA CAAAATTATA TAATCTGAAT TACATTATTC CTTAAAAACA
9901 GTTAAGTTCA TAAGGCATAT GGAAAAATAT AGGAATAAGT CATTGGTTAG
9951 ACAGTTCTGG CAAACATACT CTATGGAAAA TAAGAGTGCA ACATAGCTAC
10001 AGGGGTTATA AAATTTATAA TTCATGGTCC AAATGTACAT TTGTAGTATT
10051 GATTTTCATTG GGAATTACCA AGGGATTAGA TCAATTGTGG GGAAAGTGTA
10101 TTTTTTAAAA ATAAACAAAG ATAAAGATTT TTTTCTGAA TTCCAGGTAA
10151 AAGGCAGCAT TGCTCCTCCA TTTATTACGT AGATGCTTCT ATCAACATTC
10201 TTATTTTTGT GCTCCAAATC TTGGATTGGG AAAAATACCA ATCCGTATAA
10251 ACATAAAGAA ACCATACATG CATGTGGGGA TCCTAACACC AGAAATGACT
10301 CTGAATGCAA AAAAAAAAAA AAAAAAAAAA GGAATTTTC GTGCCCCATC
10351 CTTAGCTTTC TCTGCTTCT CTATTATATA TGCAACTGCC TGCCCCCTA
10401 TCTTACAAAG TACTTCGTAA TCTAATGCAC AGGATCAGCA GTAATGCAGC
10451 TCAGACTGCA TGCTTTCGCC TTTGGATTCC TAGATTTTCA ATTAAGGTTT
10501 AGTCAGGCTA TTGAATAGCC CTTCAATTCT AAGTGCTGAT GTGAATATCA
10551 TGCAAATATG ATGTACATAT TCCCATGTGC TGAGTAAGTA GATGTAGCAT
10601 TTGCTAATGT TGCTATACAT TTAGCATCTA AGTTATGAAC CAGATTCTAC
10651 CACTGGGTAA CATTAAAAAA AAGTTAGGGA CTTGAGGTAT GTAAAAATA
10701 GCAAATTCTA TTTCTACGAC TTTAAAGGGT ATGTGTAGAG TTCTGAAAAG
10751 AATTTCTCAG CCTCCCCCAA ATCCACATAC TTTTGAAAG CTGATGATTG

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FIGURE 3D



10801 AAAAGATTAA TGTGATCCTT TATTGTAACA TCTAACATAA TTACATTTTA
10851 TTTATTGTAG AAACCTTTATT ACCTACTCTC TCTTCCCTTT GCAGAATCAT
10901 GCTGCTTGCT GTGGCAATAT TATCACTGTA TTCAGTTCAC CTTTTATTAA
10951 AAACAGCCAA GGAAGGAGGT ATGCTACCAC TTGAGTCCAA CACATTCTAT
11001 TTTAATTCTC ATAAAAGAGT ATTTTCAGTCT GTTGCTTCAT AACCTTAGGA
11051 TGATTATAGT CAGTTTCACA TTTTCATTTTC TTCTGAGCCC AGTGACACGA
11101 TCTCTCAGTG TTTATAGTTG TTTGGGCAAG TGAGAGGCAG GAGTGAAAGT
11151 CAACTGGCTC AGGTTCAAGA CAAATAGAAA AAAGAAATTT CTGATATATG
11201 ATAGAAATAA CTGTTTTGAC TTGCTACATG CAGCTAAAAT AAATAAAACC
11251 ATTGATTCTT GTTTGGAGAA CATTTTGATA TATTGCTTAT TGGTTTTTGA
11301 GGTTGCATCT TTTGGGCTTA TAATTTCTAT ATGATGTTTA TTTACATGTT
11351 TGAGACTCCA GCATGGAATT ATATGACAAA AATATTTTAG TCATTA AAC
11401 AATCTCTTTA ACAAGGCTAT TTTATCTTTG ATTGTAGGGT CTTTGATTTA
11451 TGAAAAATTA GGAGAAAAGG CATTTGGATG GCCGGGAAAA ATTGGAGCTT
11501 TTGTTTCCAT TACAATGCAG AACATTGGAG GTAAGGGGAT ATACTTTCCA
11551 ATGGATCCCA TAACTTTCT ATAGCGTGTT CAATAAATAA GAAAACCTAT
11601 GGCAATAAAC AGGCACTTTA GATACAGAAA AATTGCTACT TATAGTTCTT
11651 AAATTTTAAA ATGATAGTTT CTAAATAGG TTTGTGTCCT GCTTTAATTA
11701 AAAACAGCAA TATCTAAGAA TGAAAATAACA TATAAAACCC TGCCAATTGA
11751 ATTCTAGAAT TAAAATATAA AATAAAAAGCT TTCTTGATT TTAATGTTAT
11801 TATAGCATGA ATTATTACTC TTA AAAAATTG AAGAATTTGT GCTTATATCT
11851 GTCATTGACA AAACAGTTGA CGTTTTCTAT GTGTGACTGA GTTCGATTTA
11901 CTAAACTGAA AAGTGGGTGT CTGGGGGAAC ATAGCCAAAT GCTGTGGTCC
11951 TTGAAACGCA GCCTGCACTG AGCCAGCCCA CTAGACAGTG TCTCTGGAAG
12001 TTTACTAAGG CAAAAGTCTG GCTAGGCATC AAATGCACTA TAAACCCCGG
12051 TTTGTTGATT CTATGGATTC TTATAATTCC CACTGAATTA TCATTTCCAG
12101 TGTAGGACCT AGAAATATAT ATATATATTT TTAACAATGT TCTCTCGTTG
12151 GTGTGTTTGC CCACCAGCTT CATACTGTTT CTGTTGTGTC TTTGGCCCTC
12201 AGAAGGCATC CAAACCCATA TTTTCAGATGT CCTGCCGGCT GCTTCCTGGC
12251 ACATGGCCCC AGCCATCTCC CCACATAATG ACACTTACTC CCTCACCTCC
12301 TACCCAGTCC CTAAACCTGC TATTCTATTT CTCTGATCTT TCTTTTCTCA
12351 GTGAATACCA CCAGCAGTCA TCCAGTTTCT GAGGGCAGAA ATCTGGATGT
12401 CAGCGTAAAT GTTTCCTTTT CCCCACCTCT GCATGTCCAA TCAAATGGCA
12451 AAGTCTGTTT ATTTGATCTC TTA CTATCT CTGAACCTC TCCTCTCTGT
12501 CCGTCCTCAT GACCACAGAT GATCACCATT TATAGCTCAG ACTATTGCAG
12551 TAGTCTTCTA ACTGGTCTTC CTGGCTTGAG TTTCCCCTGC TCTCAGATAA
12601 ACTCTAATTT GTTCTCCAGA TAACTTTTCT CAAATTTGAG TCTGTTTCTA
12651 CTTTTGTCTG GCATAAAATT CTTTCAGCATG CCTTTATTAT TTTCAAGGAA
12701 AAACCTTAAC TCATTGGACT GACACAAGAT CTTCTGCTAG TTCTTCTGCT
12751 CAATCTTTCT AAACCTTTCT AGCAATGCCC ATATCTATCT ATCTTTATCT
12801 ATCTATCTAT CTATCTATCT ATCTATCTAT CTATCTATCT ATCATCTATC
12851 AATTTATCCA TCATCTATAC CCTACATGTC CTGTGTCAA CCATAACAAA
12901 TTATATTTAT TCCCCTAACA GTA CTATTTT AATATTTTAA AAAATCATCC
12951 ATGCCTTCTT TTCACAGGCT ACTTTCTCCC CTGACTGTC TCTCAAAGTC
13001 CTCCAACCCT AACACACACG CACACACACA CACACACACA CACACACACA
13051 CACACACATT TTCTCTCTCA CTCTGCTCAC CTGGTCTATT GCTCCTCTAG
13101 ACTGGTAAAT ACTAGTTCTT CTGGGCTCTC ATGGTCTCTG TTGTATCTAG
13151 TATGTTACTG TTTTCTAAAG GATATTTTAA AACACTTGAG TAGAGAATAA
13201 GCTTTTGGAG TCTGATGGAC CTGAATTTGA GTCTGTTTCT GTCATATCT
13251 GTGAACTTGG GAAGATCACT GTA CTCTCTT GTCTGATTTT TTCATGTATA
13301 AAAATTACCT TACAAAGGCT ATTGTGAGGA TGAAATAAGG TAACATATGG
13351 CACATAATAA GTCTCTGGAG TATGCTTCTC TCCTCCCTGG TTCTCTGCTT
13401 CCATATCCAT GTCTCTGGAG TTGCCTGAAT TATTTTTTAA ATAGGCATTT
13451 AAAAAATTAT AAAACAAATA TATGATGATT GTGAAAAACT AAAACACTGC

FIGURE 3E

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13501 ATAAATATAT AAATTACCAA GAAAAGTTTA TGTCAGTCAT CCTCAGAAAT
13551 AACTACTCAT AGGTTTTCCC CTATGCCTAA TTCAACAAAT ACATTGAATA
13601 TTGTTAGTAT TGGATCATCT TATGATACCG ATTTTCAGCT TTCTTTTTAA
13651 ATTTAACAAT ATGCCTTGAA TATATTTGCA TGTTATTCTT TTTAATGATT
13701 TTTGAGGTTT CCATTACACA AATGTGCCAT AATTTGTTTA CAGTATCCTT
13751 ATTGATGAAC AGTTGGATTG TTTCTAATTT TTTACTGTTA TAAAAATGCT
13801 ACAGTAAATA CACTTGACACA GAGATCTTGC AAACAGGCAA CCCATTTTAA
13851 TAAATAAATT CACTGGAGTT ATCAAGGATT TCTGGAATGC AGAAATTTCT
13901 TTAGTAATCT ATCTAACTAT ACTCACCTG ATAATGGATA GTTGGTAAGC
13951 AGATAAGTAA AATTCAGCCA TATCTTATGA TTTGTGTTAA AAAAATTTTT
14001 ATATGTTAAG ACTACAATCT TGGGTAGAAT TTGACAGTAA TATCAAAATT
14051 GTCTCATTCA TTTTACTGGT TTGGAGCCAT ATGCATATTA GCCCCCCAAA
14101 TCCCAACAAA TAGACCACTT TACATTTGTT TCAAACCTCTC AGCCTTATCA
14151 AGGTTTAAAG TATCGAGCAT TTCATAGGAT TGCCTTATAG TTGGTCTAAT
14201 TTAACAACCTG AAATAACCAG GCATAAGCAT AATTAACCCT GGACTCAAGA
14251 AGTTGAGTGG CAGCACCTCA GCTGTGGTTC AAAGCATAGC CACTACTACG
14301 CTTCTAAACA ATGGAATAAA GTATAAAGCG GTCTCTCAGT CAAGCCTCAC
14351 ACAGGTAAGA GCGTGACTT TAAGGGAGTA AGATGAAATA TCGTAACATC
14401 ACCCCAGAAA TAATGCTCTC ACTTTGGTTA CTTTATTTGA TTAGTTGATA
14451 TTTGGCATAA GAGAAATCAC TTGTATTCTT CTATTTAACA ACTCTACATT
14501 TAGAACACTT AATTTTCTCA ATCCCCTAAA AAATTAACAT TTAGTGCAGA
14551 TGTTTTTACA TTAACAGATT AATGTCTGGA TCATTCTGAA TTTTTGAAGA
14601 CCAAACATGT TAACATCACT GACATCACTG AAAACCAGCA ATTAATAGCT
14651 GTAACATTGA ATGGTACCTC ACCAAGCCAG CTAATCAGAA ATATCTCCTG
14701 TGTTCACTCT CTGTAAGATT TAGCTTTAGC CAAGGTCTTT GCAAAGATTA
14751 ACCAAATAAT GTGTACAGAA GGTACATCCG CTATTGTAAG AATCATTTC A
14801 CTTTGACAGT ACAGAAGAAG CACCAGCCCT TCTGTTTTAG ATGTAGTCCG
14851 TCCTTTTCAA GCTGTATGAT TGTGGACATG TCAACTTAAC ATCTCGGAGT
14901 TTTTATATCT TCATCAGTGG AATGAGAATA ACAACATATA TCTTGTCA TC
14951 TCACAGGGTT TTTTATCATC TCAAAATGAAG TAATGTGCAG AACTAACCAA
15001 TGTGGGGAAT TATTATCATC ACTGTTACTT TCATATGAAG TGAAGAAAAT
15051 ATTTTTTAAAC TCAGTAGTTT AATTTACAAT TTAAGTATGT GTTTTTAAAGT
15101 GCCTGTTAGC AAAAATTAC TAGAAGGATG TAGGACACAC TTAAAGTTTT
15151 CATGTAAAT TTGTGAGTTC TATTTTTAAC TGAATCTTTT GGCCATGTGT
15201 CAACAAATTA ACGTTATCCT TCACCAAATG GGTGGGCTTG AAAAAGGCGT
15251 GATGCATAAA TATTTACAGT TGTAGGCAA ATTGTAATGT TATGTATATG
15301 AATACATATT CATTTTTTCA GGGAGAAGGC TTGTAGATT CATCAAGAAA
15351 TCTTTCACAA GAGTAGATAA TCATTCATGT ATCACTTACC TAGATGCTCA
15401 TGAAATTTTG CCACTTTATA TAATTCCTTA GTTAGCCAAA AGGAGAGTAA
15451 GATGAAGAGG GGGGAAAAAA AAAACTTCTT TGACAAAGAT GGAGAGAAGC
15501 TGTCATCTCT TGTATTCTTT TATCAATCCA GGAAGCCTTT GGTTTTGACA
15551 ATAAGTGGTC TGAGACTTTG TGTAATCCTC AGATAGGTCC CGGAGGACTA
15601 GATTGGTGCC CATCTGCAGA AAACCAGAGG GGATATATTG ACTCTGCAGA
15651 TCTGCCCTTT GATTCTGCCA TCTCTCAGCT GGCCCATGCC TTTTGTGACC
15701 AGACTACTGC CCAAGTTATA GACACTAACA CAGGCACACT GAGTATGGGC
15751 TATGTTGATT TATAACTAAT GAGGGCAGAA CCTTAGAACT GCAGCTTCAC
15801 TGTAACCTTT GGAGCAGGAT TTAACACAGA ATCAGCCCTG ATACTGTTAA
15851 CAAAGGTCCA CCTGAAAGAG CTGGAAGGTC AAATGTCTAT CTTGGAAGAG
15901 AACTTGGAAG CAGTGCCAAA TACACAATGA CTTTTTTTTT CATTTGGGGG
15951 ATTAGATGTT CATCTTACAT ATCCCAAATG TCATAACTTG CTTGCATGTG
16001 ACTTCAGTAC TGTCCACACC ATTAAGCTGT CACATTTTCC ATTTTAGCAA
16051 TGTCAAGCTA CCTCTTTATC ATTAATATAT AACTACCTGA AGTAATCAGA
16101 GCATTCAATG GACTTGAAGA AAATACTGGG TATGTCTTAT GCTCCCTCTG
16151 TGACATCAAG TGACTCATTC TACTTGGTCT TTTCTGATT TAATATCCCT

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FIGURE 3F



16201 GTCTCTCACT TCTAGAGAAT GGTACCTCAA TGGCAACTAC CTCATCATAT
16251 TTGTGTCTGT TGGAAATTATT CTTCACCTTT CGCTCCTTAA AAATTTAGGT
16301 AAAGATATTT TCTAACTGGA AATATTTTTTA TTTTATTTTC ACATTTAAAT
16351 AGGTTAGCTA ATTGTAGATG CCATATTCAC CTCCAAAAT GCTTCTTCTA
16401 ACTTCTAGGT TATCTTGGCT ATACCAGTGG ATTTTCTCTT ACCTGCATGG
16451 TGTTTTTTGT TAGTGTGGTA AGTGATGTGA TGACATGATC CTTGCAGGTT
16501 GGTTAGCATG AGTTTTTTTG TGCCTAAATT AGTGTCTCA TTTTGTTCAA
16551 GCACTTCACT AATATGAAAT AGTTCTTGTA TCACAAGTGA TTTTCTTGTA
16601 GACTAATTTA GAGCAAAAAA AGAGCAGCTA CGATTTAAAG ATAGTTGAGG
16651 TAGAATATCA AAGCTACTAC TAATGGTTTG GTCTAGGCAC ACTGGTTATA
16701 TATGGGAAA AAAGGAAAAC TTCAAGCAGG AACATGACAA TAATCTGGCA
16751 TTTAGAACAG CAGAGGAGAG TCCCAGATGA GAAACAAGAA GGCTATATCC
16801 ATATTCACAT GAATCAGCCA TTCTCTCTTA CACATTCCAC CCATTAAGAG
16851 AGGACAAGAA CAGTGGGATT AAAGAAGAAA TCCTCCTCTC TAGGCCCTG
16901 ACAAAGAGG GAATTTCTTG CACTATCATG AATGCCAAAA TTTATAAAGC
16951 ATTTCCCAA AGAGGTAAAG GAGAAGGAAA AAAAGTTTGT AAGACCCATG
17001 TCACCTTAGT TTGAAGAAAT AAGGAAATGA TCATCTTCT CATGGAAGGG
17051 CATGAAAGAG GGTGGGAAGG ATTCTTGCAA AATATTGTCC TGTAACTCT
17101 AAGAGGCAGG GCTGCCAATC ACAGCTCCAA CTCTTCCCTT AGAACAGAGG
17151 CTAGAGGAAG TTTACTTTGT CCATTAGTCT AAAAGGAATC CCTAACTGAG
17201 TTCCCTCACC CCCCACCCTA TAAGCCACAC ATATGGATT CTTATTCATT
17251 GTTTTTTCTC AAAAAGCTGA TTTTTTTTTT TTTTTAATG ACTGAGTCTA
17301 GGTGATTTAC AAGAAATTCC AAATACCCTG CCCTCTACCT GTTTTGATC
17351 ACAGTGTTGG AAATCTGTCA TTCAACAACA CGCTTCCAAT GCATGTGGTA
17401 ATGTTACCCA ACAACTCTGA GAGTTCTGAT GTGAACCTCA TGATGGATTA
17451 CACCCACCGC AATCCTGCAG GGCTGGATGA GAACCAGGCC AAGGGCTCTC
17501 TTCATGACAG TGGAGTAGAA TATGAAGCTC ATAGTGATGA CAAGTGTGAA
17551 CCCAAATACT TTGTATTCAA CTCCCGGTA AGTGAGCGGT CCGGGCTTCT
17601 AATGAGTACA GTTATGTGTT TTCTAAGTTT TTATTCAATA AACTGAGATG
17651 GCCTGAGATC ACCATCTATG TTGGAATGCT AAACACGTGG TGTGTCTTT
17701 GTTTTTCAGA CGGCCTATGC AATTCCTATC CTAGTATTTG CTTTTGTATG
17751 CCACCCTGAG GTCCTTCCCA TCTACAGTGA ACTTAAAGAG TAAGGCAGCC
17801 ATCATTTTAG CATTCTAATT TGCTTTGAAA TTCTGCTCAT ATGTTCAAAG
17851 ATTCTTTAAC AGGAAACACA GTTTATAGCT TCCTCTTCAG AGAAAAATATG
17901 TACTCCATCC ACTCCTCAGT AACATGCTTT AATCAGAAAG GTGGGAATCA
17951 GCCCACCACA GCACTACCTT ATCTTCTTTC TCTCCTTCT CTCCACCATA
18001 ATGGTTCAGG GGAGGGGTTT ATGGCAGGTG GACAAGGAGT CGATGGTTGT
18051 AATAATTTTG GCAGGTGTTG GGAATTTAAA TTTGAATTT GTTCGGAAGA
18101 AATGATGTCA GCTGGACTAG AAATGAAAAC ACCCATGACG ACCAAAACTT
18151 ATGGTTAGGG GCAGCCTCGA TAAGCCAGTG ATGTCATTTA TAGTCAGCAC
18201 CTAACCCTTG TCTAGAACAC ATTCATTACA AGAGATGTGT CAATATCTGT
18251 CCTTTGTTGT CTTATTTGTA CAATAGAGTC ACTGGCTAGA AAATCTTGT
18301 TCTTCAGCT GATGGTCTAT GGTTCATTTG TATCTTTTC CCTTTGAAGT
18351 TGTTGATATT TGCTTGGGAA CAAAGGATAT GAACTCATT TAGCTGTTTT
18401 CCTCTTCTT TTAAGGGAGG ATATTATATA ATAATTCTCA ACTTCTTTAA
18451 TCTAGACATC AGTAACCTCA GTCTTCATTC TACTAAATA GCAAACTTT
18501 CCCATAAAT TCTGATTTAC CTCATAAAAA ATTTCAGAAC ACTTTCAAGT
18551 ATTTTGATGT CTTTGATTTA CTTTGAAAAT TACATGTAGC AGTTACTCCA
18601 GAAGCCTGAC AATTGATCTT TGGCAGCCAG GTTCCTTCTA GAATGGTTTT
18651 CAGAAGCTTT TCAGGTAGTC TGGACTCCTG GCAGTAGTAC TTTGCTGACT
18701 CTAAGGTT CTTTTCTCA TTTAAAGTCA TCTCATTATG AAATGCAAAA
18751 GCTTTCTATG TTAGGAGCCT GTTTCATCTT TATGTTAATT ATATTCTTAT
18801 TCAGTGGGCA AGCTTACTGA CCTACGTGAA ATAGACTGTT CCTCTTCTAG
18851 GGAAATGATT GTTTTTAAGA CTGAAGGACT AGTGTTTAAG AAAAATGGAA

FIGURE 3G

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18901 ATGAATCCTC ATTAGCTCTC TAAGACAAAT TTAAATCAGC TATAAGTTTA
18951 TGTACTAAAT ATGTCTTCAT GATTAGCAAT ATAGATATAC TTTTTTATTA
19001 TTATTTTCAT TTTGAAAAGT GATTTTTTTT TGTAAGTTTA AAAAACAAAG
19051 CTTGGTGTTT TTTCTTTTTT CAGTCGGTCC CGGAGAAAAA TGCAAAACGGT
19101 GTCAAATATT TCCATCACGG GGATGCTTGT CATGTACCTG CTTGCCGCCC
19151 TCTTTGGTTA CCTAACCTTC TATGGTAGGT CACTCTGAAA GTCATTCTCT
19201 ATATGCAAAT CTTGTITAGG CTGGTCCTTG ACCTGGGTAG GTATGATTTT
19251 TAAAAATTGC CTTCTATAAG CATGCTCTAT AGATGACACA TATTCAATTA
19301 ATATACTATT TTAGTTTTGT CACTTGACCT GAGGAAATGG GGCCTGATTC
19351 AGCCTGGCTA ACAAGTTACA AGAATTTGTG AATTAACACC TATTTTATAA
19401 AAAATATCCC TCAAACAAAA TTATTTTCCT CTAGGGATAG ATGATATTTT
19451 TCTGGCTAGA CTCCATAGTC CAACTCAGGC TACAAGTGAT GAGAATGAAT
19501 CCACTTGCAT GTGATAAAGC TCCTTTGATG GAATTATTA CTGCCACACA
19551 AATAGCAGGG AAAGTCCAG GTCCTCAAGT TTGAATTTGC CTCCTCTTTA
19601 CCACTCAAGT CAAATCTGGG AGCTTGGGAC TTTAGGTAAA ATTTCTGACA
19651 TATCCCATTC TATTTTGTTA TACTAAATGA TTTCTAAGA AAGAGGACAT
19701 GACAGAATTT CCTTCAATCT AAGAATGCAC CACCAAAAAA AAGTGACTAT
19751 GGCCACATTA GATTATGCCT GCAACATTTT CTCTCTGGCA TCTTAACAGT
19801 TCACAAAGGG AGTAGGATTG TACTCCTTCC ATGAAGTGTG GCCACATAAA
19851 CAGATTTTAT GGAATCACAT ATTGACCTGG TAGCATATGT TTACATGAAT
19901 CAGTGTATCA ATATAAATAT ATTTTGTAT AAACCTCCTT TTAAAGTTTT
19951 TAACTTAATT TTTTCTTAC TGACTTGGTA AATTGAATTG CATGTATGAC
20001 AAATTGTGGA GGAAAAGATT CAGGAGTAGG CCACCATTGT CTTAGGTTTT
20051 TTTTCTATTT GACTAATATT TGACTATTAA CCAAACATGT GCTTTAGATT
20101 GGGCATTAACT TTTTGGCCGG TTGTGAAATA ATGAATGACG AGGTCAATAC
20151 TACTGAAGGT ATTTTCACTA CTTTTGTCT GATCTTGAGG TGAAAATCCA
20201 ACTACGCTTG ATTCCATAGA TATTTTCTTG TTATTTGTGC TTGGAGTCCT
20251 GAATGAAGGT GTTTTCAAGT AGGGCTGCAT CTTCGTCTTA GAGTAGTACC
20301 CACTGGGAGA CCATCTAAAA ATTATACTAA TTTATCCCTG CACGTTACTT
20351 ATACTTATTT TAATGAGTTT CATAAGACAA GCAAAAACTT GAAAGAGCCC
20401 AAAAAATATCT GTTTTAGTGT GGTGATGGAG TCATAGTTGT TGAGCTTGAA
20451 AAAATGGTAG CAATCATTCA TCCTAGAGTT TACACACTGG GTTTGTAACC
20501 TGCATCAGGA GTGGCTGCAC AGGTAGGGAC AGGGGAGGTG GTAGGCTGGG
20551 AGAGACAATA TGTGGGGCTT GGGTCTCTCA TCCCCTTCAA CAAGAGCACC
20601 TTGGTCTCTG TCTGATTTGT AATTGCTTCT GTACAGCGGA GATAGATTTA
20651 TCACAATGTA AATGAGCTTG AGAGGCTCTT TATTTTGTAT TATACCTTCT
20701 GCAACGTTAT CAGCTTCAGG ACCTCTTTGT TCATTTGAAT GAAGGTTGCA
20751 TAGCTAATGA GCTCAGAGGC AAGACCAGAG GTGCCTGGAT TCCCAGGCCT
20801 AGGTCTTTTC CTCTGTTCTG TGTTCTCTCT ATAAAATGTT GCCATAAGTG
20851 ACCTGTGCTG ATTTGACAAC ACCAAGCGGT TTCACTTCTT TTTTCTGTT
20901 GTAGGAGAAG TTGAAGATGA ATTACTTCAT GCCTACAGCA AAGTGATATC
20951 ATTAGACATC CCTCTTCTCA TGGTTCGCCT GGCAGTCCTT GTGGCAGTAA
21001 CACTAACTGT GCCCATTGTC CTCTTCCCAG TAAGTACATA AGACTTTGAT
21051 GAAAGAAACC TACTTGACCC CATAAATTAG TACATGTGTT CTACCTTCAT
21101 TTTGATTTAA TTATAGGGTG AGTTTGCAAT TGCAATGCCT GAGGATATTA
21151 TTTTCTATA GCATTTTGAG TCACTTAAAA TTGGCCATTT AATGTGTAGA
21201 TAGAGCAAGT AGTTTCAGGT GGTATTTTTA TAGTGTAGGA AAAAAATCAT
21251 AAAACTTATT TTTAACTCA AAGTTGAAAA GTGGAGCTGG AGCTTCTGTC
21301 TTGTGGATTA GTAAAACCTGA GTAGGAGTTC ATATAACTTT GGAACCTTGA
21351 AAGCCAAAAC CATATTAACCT TTCAAATCTT ATTAATTTTC ATCAGATTTT
21401 TGAAGGCATT TCATTTTTTT TCCAGTTTGT TGTGCTGCAA TAATATACAA
21451 AAGTTGCCTT TTTTAACCTG ATGCCTTGAA GGCTAATGAA AAGGGGATTC
21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTTTTCAAAA AACAGTTATG
21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA

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FIGURE 3H



21601 GGTCACCCCT CCCTGGCATT TGTCATTGGT GTCAGTTTGT TCTGAGATCC
21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTGTGAGTT AAAACCACCA
21701 CCTAAGGATA AACACAGGTC TTCACCCTCC TGCCAGCTCC TGTTCATATA
21751 ACACTGAATT TACTCATTCA TTTGAGGGGG AAAAAAATAA GTGACACAGT
21801 AACCAGCACT GTCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
21851 ACTATTTCTA TAATGACACT GTGGTCACTT TAAATGCAGC TTGTGTGCTG
21901 AAATATATTT TGGCACATTC CTTTTTCATG AGTGCATGAA ATCAGATCCG
21951 TACTACTATG GTGGCTAATA TTTTACTCTT AAATCATGTC TTGCCTCTAA
22001 TATATCTGAA AGTATTTTCA ATGACATACA CATAGCTTTA GCCTAAAAATC
22051 AGCTCCGTCT TGGGTACAAG ACAGAAGACA ACTATAAACA GAAGGTATAC
22101 GATAGGGTAA AATTGCCAGG CAAACAACCT CACTGAGAAA AGGATATCTG
22151 GAGCCCTTCT TTTTATGTGT AAAAAAATCA CTCATAAAT TTTGGCACAG
22201 TGTAAGCATT CACATCATTG TAGAATCAAA GCATAAGAAA TCTGTGATGT
22251 GCTTCTGTAT TGCTTTATTC ATATTCATAT AGTGTTTTCA AGCCATGGTT
22301 TTAAGGGATT GCCAGAATTG GCCATCGTCA CACAGACAGC TGGTAACAGT
22351 TCAACTAGTG CAGCTCATAG CCCAACACTG AGGGCTGCAA TTATTGTCAT
22401 GGGAAGTAAA AGTCATTTAC TGATGAACAT TTCACCTCAG CATGGAAAAT
22451 CCAAATCTCC CCTTAGAAAT TCTTACCCTA TGTGAGAAAT AAAGCACTGA
22501 TATAAATCTG ACCATCAGGA ACAGCAATAG TGTGTAAACA TTAGATGCCA
22551 TTAGAACCAA AATTGACCAT AAGAACCAGA GTTCAGAAAA ATGACTAACT
22601 GCTGTCCTTC ATTATGTATT TCCAATCAAC ATTAGCATTT ATGAAACATT
22651 TTGCACATTA TCCTGTCCTC ACCCTTGCAA TGTTACATTT ATATAATCTG
22701 TGTAAGTGCT CCACTGCCCC ACAGAGTCAT AAGTCCCTGG GACTTGGTGA
22751 TGTGCACAGT GACTGGCACA GAGGGTGAGC TCTGTCGTGC TTGGGAAGAA
22801 AAATGGTCTT CAAATGAATC TTGCCTTGTC TTGAAATGTA TAAACTGCCT
22851 TTTCTAGCAA AAGCATAGAC ACTCTTTCCC TTGGTGACAT GTGCTACGAA
22901 TTCAGCTGGG TTGAGGATCT GGGCTAAATG AACCACCTT CCCTATACAT
22951 GAAGGATACA CAGAGATGGT GACAGAGAGT GGTCACTTCC GTGAGTGGAT
23001 CTCAATCAAG TCCTCTGAAG CTAATTTCAA TTTTTTTTCT TTAATAAAAT
23051 GATAAAAGTT GTTATTGGCG CTTTTGCTTG TTTATTTCTG ATAACCTAGG
23101 GCTCAGATTT TCAATGTGTC AAATGCTGAC TCACAGCATG GTTCTCCTGA
23151 CAGTTTATTT CATTTAAGGA ACTCTTCACC AGTAAGTTTA TTTACTTGCC
23201 TTGATATCTC CACACATTAA TAATAAAACT AACAAAACCT AATCTGAATT
23251 AAAATCTATC AGCTTTAGGC ATTATTTTGT GTTCTCCTTC TTTCAACATG
23301 GTAAGTGGG TCTCTTTCTT AGGAGCTTGA GAAGATATGA CTGGGGTTTG
23351 TTTTCTCTA CTTCAATTTAT TATCTTTCTT TTTTCCAATC AGGTTAGTTT
23401 TTTCTTTTT AGTAAAAGGT GCATAGTAAC TGCTTGAGT ATTGTGTGAA
23451 CAAGTGAATA AATGAAATGA ATTAAGGTAG TGTTTTCACT AGCAGCCCAA
23501 CATTTCTTTC TCTCTAGTA GTGGGTGGGG TATCAGTTAT GGAATGGCAC
23551 CTCCTTCCAG AGGACTGATC ATGTCATTTT CAGCTTATGC TTCCCTTTAT
23601 GCAGTAAAGT TTCCATATTT CCATAAAGAA CAAGAAACCA AATAATCCTA
23651 ATGGATATAT AATGAACACA CAGATGAAAA TTTCACCTGC CATGCCTTTG
23701 AAAAAAGATC CCTAGCTACT TGTATTTTCA CTTATAATTA AAATCAGTCT
23751 TTTCACTTAT GTTTTCTTCA GATCTCCTGT TTTGAAGTGT ATATAGATAT
23801 CAACATAGAA ATGCAGCGTA TATTGCTATC AACTGCAGTG GAGCAGTGAT
23851 TCGTAGGTTT TCCAACATCC TTGCCTTAAG CAAACCTGCA AAATCAAAGT
23901 GTGAGCTACG TCTAAACAAT GGGAGAGGCT TTTTTTTTTT TTTTAAGAGT
23951 TAGAACTAAG ACTCTCACTT CCTCCTGTGC CTCCACATTT TTGACCTTCA
24001 CATTGGGCCC CTGCATCAGA ATACAGCACC CCCTAACAGG CTCCTGTTCA
24051 GGAATCTTTC TCTGGAAATA ACAGATGTTG TCTCTAGAGC TGCATAGAAC
24101 CTTAATGGAA TCATTGTGGG TCAGAGGCC TGGATGGTGC TGGGGACCTC
24151 CCTGACCCAC AGCATCTGAC CCACATTTCC AGGTTCTTAG CGACTTGTGT
24201 CAGTAAAGAA AAAGGCACAT AGCTAAGTGG AAGAGCAGAT GAGGCTTGGT
24251 GGAATCAGC CAGTGGTCTG CCCTAGCAAA GGTAACAGA ACTGCTGGGG

FIGURE 3I

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24301 GCTTTTGGTC CTAGGCTCAC TACTCAGGGA GGCACTTTAA CATGGAATGA
24351 CCAGCAAGTT TCCTTCCTGA TCTTTTCCAC CACCACCACA AGCCTAGTAC
24401 CTCCCTCCCT CTTTGCTCTG TTGCTCTCTT CGGGAATGCA CTGGAAACCA
24451 CCTTCAGTTC TGTITGGAAT TTTCTTATTC CTTATTGAGA AAGAGGAAGA
24501 AGCTTTTGCA TTTACTCCAA CCGTTCTACC TATTATTCCC ATAAACTTTC
24551 TGTGATCTCA TATCATTAGG CCAAATGTTA ATCTTTCTGG GAGCCAGGAG
24601 ACTGCTTTCA CATTAGAGG CCCTGGACAT ATAGGACTGC CTCTAACTCA
24651 CTCTAACTCA GCTTATTGAC TTGAATGCAC CTTTTTAACA AGTGACTAAA
24701 AAACAAACTG TGACTATTCT CTGAAAATGA GCCTATATCT CATACTTATT
24751 TATTCTGTTT AACACTGTGA AACAAATTAA GTCCTCTGGC ACTATGTATA
24801 TACCATAAAA AGCTTATTTG TAAGCCTACT AATTGGACCA GTTTTGACAA
24851 TATTGAATAA GCACTAATTG CAGATCATAA TGTAGAATTA TAGGCTGCTG
24901 AGGAAAACAA TATCACACCA TTTGCTTTCC TCAGTTTCCT TTTCAGAATG
24951 AGTTTCATAA TGTTCACTAA TCCAATTTTT AAAATCCTTT ACAAAAGTTAT
25001 TCTTAAACTA TTTCCAGAGA CTATCTGGTT TGTCATTCTA GAAATGAAAT
25051 TGCCTTTTCA GCCTAAACAG ATGGCCTTAA TTTTGGTGG AGTGGTATGA
25101 AAGGAATGTC ACATGAGAAA CTGCAAGCTA TTTAGCTTGA ATTTTTGTC
25151 ATTCATACAT GTTTCAAAAT ATATTTTACA TTTTCTCTCT TTTAAATGAG
25201 TTCCCATCTC TGCACCTTAA GTGACTTCAG AACTAAAATT TTAAAGTGAA
25251 CATCAATCAC AGCATTTCCT AAAATGTGAA CTCCTAGCTT AACCGAAGTA
25301 TTCACCTTAT GGAAAGCTGA TAGAGTAATT CCACTAAGTC CAAAAAGTGT
25351 CCTCTAAAAG ATTCCAAAGA TAAGAGTGTT TTCAACTTTG TCAAGCTGTA
25401 CAAACACAAA TGTCCTCCC TCCCTCTGCC CACAGGGATC TTTATCCAGT
25451 TACAGCAGCG TAACTTGAGC AGCTGCTGCA AACTGAGGCT CTCTTGACCC
25501 TTCGCCTACT TATTTAGCT GCTAAAATAG GGCTGAAATC TGTCAAGGAT
25551 CCTGAAGGGA AGGATAAGAT TCCTACTATT CAATTTAATT TAAGCTTTTA
25601 TTCAGTGCCT GCTGTGTGCA CAACACTAAG CTAGAAAGTC TGAGGAATGT
25651 TTAGATTATT AGGTCTGTG CTTGCTTTT CATAGATTTA CAATCTATTG
25701 ATAGGGAGAG CTAAAAAGGA GAGAAAGAGG AAGGAGCAAA CATAAAAACG
25751 TCAAAATTTT AAAATACCAT TTTAAAATTT TATTTTAAAA TGTTAAATAC
25801 CATGCAAAAT TAAGGAAAAC CTAGATTCAT AAAAATTCCT TTCACAATCT
25851 TGTGTAAATC AATTCAGTGC TTGCCCTTAA TGTCTCATCC AGTCTGATGA
25901 GACATGTTTT GTGATCAACA AGGGTTTTAC TATGTTTCTT AATTATGTGT
25951 CTTGCCTGTT ATCTCTTTCT GACCGAGATT ATTTTAAACA ATAAATTCTG
26001 AAAACTAAGA AAGTGAAAGC ATAAAATATT GTCTTATAAA ATACGCCAAG
26051 GAAAAAATGA CACTCCATTT CAAATATCAA AAGTTAGCAT CAAGACTGCA
26101 CAAGATGAAT GTACAGTCAT GTGTTGCTTA CAAATGTGGA CATATTCTGA
26151 GAAATGCATC TTTAGGCAAT TTTGTCATTG TGCAAACACC ATAGATTGTA
26201 CTTGCAGCCT AATTGGTGGA GCCTACTATA CACTAAGGCT ATATGGCATA
26251 GCCTAGTACT CCTAGGCTAC AAACCTGTAC AGCATGTTAC TGTACTGAAT
26301 AGTGGAGGTA CCTGTAACAT AATGGTAAGT ATTTGTGTCT CCAAACGTAG
26351 AAAAGCTACT GTAAAAATAC AGTATTACAA CCTTAGGGTA TCACTGTCTT
26401 ATATGTGGTC TGTGTTGAC CGAAATGACT ATGCTTAATA CCACTGAACT
26451 GTACACTTAA AAATGGTTAA GATGGTAAAT TCTATGTTAT GTATGTTTTA
26501 TAATAATAAA AAAATTGAAA AAAGCATCAA CATCTTTTCT GGGAAAAAAG
26551 AAAAAGAAAG AAAATGCATT AGAGTGATGA GAATATTTGA AGTAATAGAT
26601 AAAGTCAAAA ACAAGAAAT GATCTTGCCT TTGAACCTTC TTGTTTAAGA
26651 TTCGTACATC AGTGATCACA CTGTTATTTT CCAAACGACC CTTGAGCTGG
26701 ATACGACATT TCCTGATTGC AGCTGTGCTT ATTGCACTTA ATAATGTTCT
26751 GGTCACTCTT GTGCCAATA TAAAAACAT CTTCGATTTC ATAGGTGAGT
26801 TTCAGAAAGG CTTCAATTTG GTCAACCCAA ACTCACGCTT CATTAAATGA
26851 TGGACAGGGA ACCAGTGCTG GGTCAATCCAG ATCCCCGTTT TTTCTCAGGC
26901 TCATGGATTCT CCTTATCCC TGCGAGGCTC TGGTGATTGA GCTGCTCACT
26951 GTCTCTTCTT CCTAACTGAC ACTGGGAGCC ACCTTATAGG TCATTTAGTC

FIGURE 3J

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TECH CENTER 1600/2900



27001 AAGCTGCTTT TTCTGATAGA TGAGGAAACT GACCCCTATA AAAGTCAAGT
27051 CATATACCTT GGTGTGGACC CAGGATTTGG ACTTAGGTAT TAGCTCCACC
27101 ATCAGGAAAA GAGGAAGATA GATTTTACCT GCCAGAAGCT CTCTGATACT
27151 ACGAGTATCA GCTGAACATT GAAAGGTATC TTCAGAGGAA TAGGAGGTTG
27201 ATTATATAAA GTGTATTATT AGTATTTCCC CATAACTGCA TGGTCTATTA
27251 ATTTTCATTG TACTCATTGA GGGTTTACTT AAACCTTTAAA CACAATCTAA
27301 AACTTTAAAA GAACCATGGG TAGGTCACCT GCAAAGTAAG AGGTGGATAG
27351 GGTGTGTCAT GAGTTCAGCC ACCTTAGTAT GTATTTATAT TACTAATCCC
27401 CTGTAAATTT GTGTTAAATT CAGCCTTTTG TTGCTTATTA TATGTTGCAT
27451 ATACTTATGC AGCTTTGATG TTAGGTACAT TTTAATTGTC TCTATAAACA
27501 TATCTTCTAT GAATAAATAA CCAAGATGAG CTTATGTGAC TTAAGTGTGT
27551 GTTTTTAGTG CTAAGTATAG GATAGCTTTA TATTTGGTTT ATTTAAAGTG
27601 TGTGCTGGCA TCTCCTTTGC TAGGAACTGC TGGGTAAGAC ATTGACCTTG
27651 CCCTGTGTTT GTCTTCTCAG GGGCTTCTTC TGCCACTATG CTGATTTTTA
27701 TTCTTCCAGC AGTTTTTTAT CTTAAACTTG TCAAGAAAGA AACTTTTAGG
27751 TCACCCCAAA AGGTCGGGGT AAGTAAACCT TGCAATTTCC CCCATTATTA
27801 GTTGTCTTC CAACTACTTA GAATAAACTA GAAAATACAC ATAGTTCAGA
27851 AAAATGAATC AATGTACAAG AACCAAAAAT CAAAAATGGG CTAGAACTTT
27901 CTGGTAGCAG AGAAAGGGGA CATATTTCTG AAACCTCAAAT GATTCTACTT
27951 CAAATATCAA ATATCCTGTG TTGAGTCTGT CATACATGTC AAATAGTAGT
28001 AGCCTTTCCC ACAGACACAT ATGCTTCAGG CAAATAGCAG TGTCCAATAC
28051 CAAGCTGCTG TTGTGCTATC CGTGGAAAAT CATGCAAGAA GGAATTAGGC
28101 TCCCTAGCGG TGTTATGGAA TAATTTAAAT ATTTTGGTCA TGGTTGTTAG
28151 GTTTGCAAAG CCAAAGGAAA GATGTTGCTT TTGTTTTCCC TTCCATAGTA
28201 CCTGTTGTCC CTGGTGTGGA CTAAGATCCA GAACAGAACC ATTCATCGTT
28251 CTGTTAACCT CTTTAGATAC AAAATACAGT CTTATTAAT TAGAGAGTAC
28301 ATATTTCTTT TCCATAAGAC TACTATAGAA ACAAATGCTA GAAATAATTG
28351 TTTTCCAAT AAGGAAATAT TATCTTTCAC TCCTTAATAA AGTCATGTTA
28401 AGGCTTGAAA AGAATATTTT TTAAGTGAAT ACTCTGAATT TTTACCTTGA
28451 AGTCATTTAC CTTTGGGATG TTCTGGGGAC TTCAGGATAA TTTGGTATCA
28501 AAAGGTCCAC CCAGCAGCTT GCTCCCAAAT TTTAACTCTA TGTAGTCCGT
28551 CTTGCTTGGA TTTTACAGC AGTGTGACCT TGGCAAATTA CTTGTCCTGT
28601 TTGTGACCTA TTTTCAGTTT GACCAATTGT GAAATGAGTA CAATTATCTC
28651 CTAGACCCAT TCTAGTGAAG AATGTTTAGT TGCTGCTTTC TTATATGTAG
28701 GATTAGGAGG TTTAAGTATG TGATAAAATG TAAGGCCTCT TCTGGTGTTA
28751 AAATGCTGAA GTATTTTATA TGTAGGTATG TACATATATC CTTATATATG
28801 TGTGTGTATA TTATATGTAT GCACACACAC ACACACATAT ATACACTTTT
28851 TGTTGCAACA TCTATTAAGC TTTTGGTTTT GTTTGCTTTA TAAAATTAGA
28901 ATCATATCAT ATATGCTATT CTTTTTTAAC CTGCTCTTTT TCACCTAAAA
28951 GATTGTAAGC ATTCTCTAGA TTATTGAATC TTTTCTGTG CTTGATTTT
29001 TAATAATCAC AGGGTATTCC ATCATCTTGG TGTACTAAAT CAATTAACCTA
29051 TTAATCCATT GTTGAACCTG TAGGTTGTAT CTCTCCACTG TATTCCTCTT
29101 CTTTCTTCAA CTAGGATTCT AAATTGACTG ATAGGTTAGG CCTGGGCATC
29151 TGAGATATTA AGAATAATAT GGCTCAATAT ATAGATCAGA TTGCCATATT
29201 ATGTAAACAA CTAAAAACA AATTGTAATA AGTATGGTTT CTGTGCTCCT
29251 AACAGAGTCT CTCTGAATTA CAGGCTTTAA TTTTCCTTGT GGTGGAATA
29301 TTCTTCATGA TTGGAAGCAT GGCACCTATT ATAATTGACT GGATTTATGA
29351 TCCTCCAAAT TCCAAGCATC ACTAACACAA GGAAAAATAC TTTCTTTTTT
29401 TATTGGAAAT GGTTACAAGT TATACTCCAA AAGATATTTG AATTATCTTG
29451 ATTGGAATGT TATTCATAGG AAATAACAGG AAGATTCCAA AGACGTTTAC
29501 CAGTAATATC ACCAGGCACC TGCAGAAGAG GAAAATCACT GTTTTGTGCA
29551 AGGATGGTTG TGTATGTGTT TAAAAATAAA CCTGTGGTGC ACATTTCTAC
29601 CCAGGTTTTG CTAGAGCAGT GTGAGATGAT GAAGGTGTAT TTTTGCTGCT
29651 TTACGAGCAG AATAAGGGTA ACTGCATGTA ACAATCATCA GATAGTACTC

FIGURE 3K

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29701 TTTCCCTGC CGTCTCCTCA TCCTGCACCC CCTAAAAAAG TACCAAACAT
29751 TTGCATTCTC AGAACATCAA ACAAAAAATGC CCTGGTGGCA AAGCTATCAC
29801 CATTTAATGT CTTCTCTCAG TCTTGCACCA AAGTCTCTGG TCTGTTTACT
29851 AACAGAGGCA AAAGGCATGT CTTAGGAACT GTTTCTGTTT CTGTAAGGTA
29901 CATGAATGGT CAAACACCAG TCTAGAGCAT CTTATTGTCA ACAGCAAAAT
29951 AATATTTTGC CCACCCTGTT TGTGACATTG AGTTGTGACT TCTATATTCA
30001 ATAGATTTTT GTAAATGTTA AAACATCTAT ATTTAAATGT TAAAAACTA
30051 AATATAGAGA GGGGCTTTAT TTCAATCATA GAGCAACAAC AAAAATAATG
30101 CTTATAGCTA AACTGCCTGT TCTAGAAAGC ATCTGCTTTT TCATGTTATT
30151 CCTAAATCCT CTTGTCATAC TTTTGTCAAT GAACAATGCT CTCCCTCTCG
30201 TCTTCCATCC TCATTAGAA TTTTGTAGAAG ACCACAATCG TGGAGATACA
30251 CTACCCAGTA TTGTTTGATA CATTTTATT TGATAAACAT TCAGTGCAGG
30301 AAAGTGTGAT TTGCTATATG TTTATGTATA TAATCTTATT CTGTAGTCAT
30351 CAGAATGTTA ATGTAAGGTA CATTTGATTT TTATTTTTTA CATGTGTAGT
30401 TTTCTTTCTT CACAGTCAA GCATTTATAT TATTGGGGGT GGGGGCAGGG
30451 AATTAAGTTG GTGGGCTCGA AAATCCATTC ATATGTATCT GTCTACAAAT
30501 GTCTGGGGAT AATTTAAATT TGAAACCTAA GTTATATATA GTTTGGCAAT
30551 GCTCTTCTTC AATATTTACA ATAATAGGAT GATCTACAAG AAAATAAGTT
30601 TCTTTTGTCA AATTTTATC ATAATAAGT TGTCTTTTA ATTTAGCATA
30651 TCTAAAATAG GAATTAGTTC AGTTTAGCTC ACACAGGTGT TTGCTGACAT
30701 TCATTGGCCA TTTAATACAG TGTGAGTGG TTCTCCGTAA AAGTATAAGT
30751 GCTAACACTA CGAAGAAATG CACACGATCA TTCTTGCTCA CTTCTATAAC
30801 AAAGTTACAT AAAATGGATT TAAAAATTCC TACTCACAGC CTAAGACTTC
30851 TGGAGTTCAC TACCTTTTTT TCAAATCATA GTAAGATCAC TTGTGTATTT
30901 TATATTTTAG TAAAGCCAAT TATGAAGTAC AAGTATCATA CACGTACTTT
30951 TGAGCTACTA TTATTTGAAA AAAATCTGCC AAATAGCATC TTTAGGATAT
31001 ATTTACATTT TCACTCATCT AAAAAAGTATA CAAAAATAAA AAGTGGAAAA
31051 AGGTATCTTC TGAATGTTCA AGAGCATCCT ATAGTGCCAA ATAATAAAGC
31101 ACCATTTTTT TCTTCATAAC CAGGATTAAA ATTCATATAT ACTGCAGGGC
31151 AGACATACAT ATGATAGCTT GTGCTGATTA ATTTAACCCC ATTTGTA AAC
31201 AGATGAAAAT TTTATTTTCT TATTTTCAATTA ATAAGATGGC TCAATGTATT
31251 GGGAGGCTTC TTTTATTATTA CAGAAAGTGT ATATTGGTAT ATAATAAATG
31301 AACTTTTCAA ATGACTATGA TGTGATTTTT GATCTATTGT TAAAGAATGT
31351 TGTGTTATTT GTCCATGAAA CAAAAATTTAA AATCCAAATA CTGTCTTTCT
31401 TATATTGGTT TATGTTCCAT TTTCATTGTT ACCTTTGACA CATAACTAAC
31451 ATCTATAGCC ATCATCCTGA AAATAATTGC CATCTTATTT TGGCAAAATA
31501 GATATTTAAT CCTAAATTAT TATGATGATT ATAATTTTGG CATCACATAT
31551 ATACCACCTA GAATGAATGT GGAAGAAATG AGTCTTTTAT GGTTAGTTTG
31601 AAAGAATCCA TTGAAGATAG AAAATGAGAG AATAGAAGAA ACCTGAGAAT
31651 AGTAAAATAA AGAGCAGAGA AAATATGGGG GCAGGGAAAA CATGTGAGTG
31701 CTAAGGATTG ATTATGAATG AACGATTAGG GGGATTGATG GATCACAGGG
31751 TAAGTATATG CTTAACTTTA TAAGAAACTT CCACATAGTT TTCCACAGTG
31801 TTTCTACCAT TTTCAATTTCC ACCCGTACTA CCTACAACCT CCACTGACTC
31851 CACAGCCCTG CCAACATTTG GTGTTGTCTT TTGCATTTTA GCCTTTCTAG
31901 TGGGTCTGAA ATGGTAACTC ATTGTGATTT TCATTTCTGC TTCTGTGACA
31951 ACTAATGTTG AAAACTTTTC AAGTGTTTAA TGGTCACTCA TATATCTTCT
32001 TTTGTGAAGT GTGTATTCAA ATCTTTTGCC CATTTTAAAA ATTTAGGTTA
32051 TGTGTTTTTA TTGGGTATTT GTAGAAGCTC TTTAAATATG GATCCATGTC
32101 CAGATTGCCA ATATATTTTC CCAGTCTATG GTATGGTTGC TTATTTTCTT
32151 AAAGGTGTCT TAATTACATC TTTCTGGGGC CAGGTCACCA TAGCTCAAAG
32201 TTTTGCAATT TATGTCTTAA TGAGATAATA TTAATCAGAG TGGTATAGTC
32251 AAAATTAATG GTTTTGATGT CCTGGGCCCC TATAGGTAGG ACTGGATCAT
32301 CTAACCAAGA TGCAAAAAA AAAAAACAAA AAAACAAAAA TAGTACTTGG
32351 AAAAATTAT TTTAAATTAA ACA (SEQ ID NO:3)

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FIGURE 3L



FEATURES:

Start: 3000
 Exon: 3000-3118
 Intron: 3119-7452
 Exon: 7453-7543
 Intron: 7544-8039
 Exon: 8040-8155
 Intron: 8156-10894
 Exon: 10895-10968
 Intron: 10969-11437
 Exon: 11438-11530
 Intron: 11531-16047
 Exon: 16048-16129
 Intron: 16130-16215
 Exon: 16216-16298
 Intron: 16299-16408
 Exon: 16409-16467
 Intron: 16468-17301
 Exon: 17302-17577
 Intron: 17578-17709
 Exon: 17710-17789
 Intron: 17790-19073
 Exon: 19074-19174
 Intron: 19175-20904
 Exon: 20905-21029
 Intron: 21030-26649
 Exon: 26650-26794
 Intron: 26795-27670
 Exon: 27671-27768
 Intron: 27769-29273
 Exon: 29274-29372
 Stop: 29373

CHROMOSOME MAP POSITION:
 Chromosome 12

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1386	T	C	Beyond ORF(5')			
2594	T	C	Beyond ORF(5')			
2757	G	T	Beyond ORF(5')			
6107	C	T	Intron			
6392	T	C	Intron			
9484	C	G	Intron			
10280	A	G	Intron			
10297	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11548	T	C	Intron			
11917	G	T	Intron			
12840	T	-	Intron			
12844	A	-	Intron			

FIGURE 3M

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Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



12847	T	-	Intron
13019	C	-	Intron
13022	A	G	Intron
13285	G	A	Intron
14461	G	C	Intron
15464	-	G	Intron
15469	-	A	Intron
15545	T	C	Intron
16199	T	C	Intron
16798	T	C	Intron
18103	C	T	Intron
18421	A	G	Intron
18528	G	A	Intron
18722	T	C	Intron
18775	C	G	Intron
18951	T	C	Intron
18974	T	G	Intron
19540	A	C	Intron
19841	G	A	Intron
20170	A	C	Intron
20343	T	C	Intron
20519	G	A	Intron
20963	T	C	Exon
21840	G	T	Intron
22783	C	T	Intron
22787	G	A	Intron
22825	T	C	Intron
22967	A	T	Intron
23248	A	G	Intron
23764	G	T	Intron
23765	C	T	Intron
24432	A	G	Intron
24538	C	G	Intron
24693	T	C	Intron
24819	C	T	Intron
25743	C	T	Intron
26044	G	C	Intron
26555	G	A	Intron
27886	A	C	Intron
31884	T	C	Beyond ORF(3')
32229	T	A	Beyond ORF(3')

411

P

P

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Context:

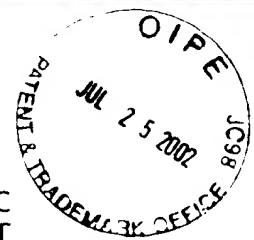
DNA

Position

1386

ACCCATATGCATGTCTTACTTCTATTCTCTCTTAGCTTTTAACTGCTTCTTTTCATCTT
 TTATGTATATACATTTAGGCTGCCTTATATTAATAATAGTTTCATTTTGTTCCTCCTGC
 TTAACCACTGTGTGCTATTTTAAATTCTGAGAACTGCTTCTTTATTCTAGACAA
 TTCTCTGCCATTATCTCTTTCTGTTTTGTCTCACCCTAGTCTCACAATTCTCTATATTGG
 AATGACTATCAGTGTATATTTGAACTTGTAATTCTTATTTTTTCCCCATTCTCTTAACT
 [T,C]
 CTTATTTGTATTTTTCTTTTTTAACTCTTTCATGCTATAATTTGAGTGATTTCACAGA
 TCTGTCTTTCAATTTTATAAGTCTTCCTTCAGCTGAGTTTTTTAAATTTCAATGATTCT

FIGURE 3N



ATTTTTTCTTTTTTTAAGAATTCCTTTTTTGACTCTTTTTGCAACAGCCTGTTCTCC
TTTTATATTCCTTTATAATGTTTTATTCTGTGAAAGTTATTCTCTTATTTTGAATGTTT
TCTTTCAAAATGTCTTTCTTTTTATTAATTTAATGTAAAAGTCCCTTTTAAATTGCTTTG
SEQ ID NO: 6

2594 CTGAACCTTTCTTTTGTTACTATTCTTAACTTTGGCTTCAGGATCCAAGTGCTAGAAAAGT
TACTTCCTAAACTTGATCCTCACCTATGTTGCATATTATCAAGCATTTGGTGGTGTTAAT
TCTTTCATGTCCAATTAAATTAAAGCAGTAATTTCTTTCTAGTTATTGCTAGTAGAGAC
ACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATTTACTTTTGCTTCCTTT
CTTTTAAACATGTATCCCACTCACAATACCTAAATTTCTTGAAGACTGCTGCCATGT
[T,C]
TTAAGATTTCTTTTTTTTCCATAGTGACTAGTAAAACCTGCCATTTTCATTATACATAG
GCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATTTCTTTCTTCTCTCCAT
TTCTTCTTTCTTGATTGGGTAAAGGAACATTTCAGGATTTGCTTATGTAAAGTTTTCA
GGAGTTTCTTTCTTCTCCCTTTTACAGAGAGCATACAAAATGTAGATGATTCATATTC
ACTTATTTCAATTAATAAAATTATAATGATGTATGTTGTGTTCTGTTGCAGAACAGAG
SEQ ID NO: 7

2757 TTATTGCTAGTAGAGACACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATT
TACTTTTGCTTCTTTCTTTTAAACATGTATCCCACTCACAATACCTAAATTTCTTT
GAAGACTGCTGCCATGTTTAAAGATTTCTTTTTTTTCCATAGTGACTAGTAAAACCTGC
CATTTTCATTATACATAGGCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATT
TCTTTCTTCTTCCATTTCTTCTTTCTTGATTGGGTAAAGGAACATTTCAGGATTT
[G,T]
CTTATGTAAAGTTTTCAGGAGTTTCTTTCTTCTCCCTTTTACAGAGAGCATACAAAAT
GTAGATGATTCATATTCATTATTTAAATAAAATTATAATGATGTATGTTGTGTT
CTGTTTGCAGAACAGAGTGTCTGAACATCAACACAAAGTGAAGAACCTTAAGCTGAAG
GTACAGTATATTATTTACACTGAAGGGGCTTGTTGTGGACAAGAAAGCGCTGACAGCTC
AAATGGATCCCATGGAAGTGAAGAAATGTCAACATCGAACCAGATGATGAGAGCAGCAGTG
SEQ ID NO: 8

6107 GTTTCGTGTGCTGTTTCTATCTACATCTCATACTGTTTTCTATTCTCAAAAAGTAACCCT
GTCATCCTCTTTCTCTCCAGATTATTTTTCAGGATTAGCTTCTGTTATAAAAAATAGCTT
GTACAGATCTCCTACAATAATTATTTTCTATTTTATTTCTAAGGTTTATTTATTTATTTA
TTGAGACAGACAGAGTTTCACTCTTGTTGGCCCATGCTGGAGTGCAATGGTGCAATCTCGG
CTCACTGCAACCTCTGCCTCCAGGTTCAAGCGATTCTCTGCTTCAGCCTCCTGAGTAG
[C,T]
TGGGATTACAGGCGCTGCCACCACACTCGGCTAACTTTTTGTATTTCTAGTAGAGACGA
AGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTTATCCACCCACCT
CAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTCTAGGATTAT
ATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTCTTTTCATGTAGGAAAT
GTCCTAAAATTTTCAACCCTCAATTTGAAAGCACTTTTAAATCATACATAGTCGAGCA
SEQ ID NO: 9

6392 CAGCCTCCTGAGTAGCTGGGATTACAGGCGCTGCCACCACACTCGGCTAACTTTTTGT
TTTCTAGTAGAGACGAAGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCA
AGTTATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCC
TGGCCTCTAGGATTATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTT
TTTTCATGTAGGAAATGTCCTAAAATTTTCAACCCTCAATTTGAAAGCACTTTTAAAT
[T,C]
ATACATAGTCGAGCATTTTATATAAAAACAACTAAAAAGTCTGTGACATTTTGCAGTATA
AAAATGCAATGGCAGCAGCAGGCTTATTAATTGAGCCTCTTGGAAATGTGGCTGGTCT
AGGTCCGTAGCCTCAAAGGCCCTGGCTTGTAAGTGCAGGAGCTGACCAGCACAGCTCTAT
AACCAAGTTGTACATCTTCTAGCCTGTGTCCAAGAAAACCAGAATCACAACGCTCTGTGG
ATAGTGACATCTTAAAGTTTTCTTTCCCTCCCAACTCTTTTGCCAGTTCATTGAATTGCT
SEQ ID NO: 10

9484 GCAACATTTATATCACAATATGTGCTGTTTATGTTCTGAATATCATATGATTAGTAA
TCACACAGCTATTTGAGGGCTAAGCATCAGGACTATAAATATTTGTATTGTGTTAGTGCT

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FIGURE 30



TTGATTGAACTCTTTTATGTATAATATTCTTCAGCTGAATGGGTTTTATATCAACTTTA
CTTTTATATAAGCCATGTTTTGAAATAAACTAGGATTTTAATAATCTGAATTTTAATAGC
TATGTATGTAGTCATATATTTGTATGCTTTTGTAAATGTGCTTACCTCTAAGACAAAAAAA
[C,G]

CTGCCCTTTCCTTATTAATTATACATACCATTAAAATGAATTAGGAAGTTACAGATCACTG
ATGAATAGAAATAGGAAAAAATCTCCCAATCCCACAGTCATAGATCATCTTCATGAGAG
AAGAATGTTCCACTTTTTAAATGAGGGCCTCATTTTAGGCTTATAAACACTTAGCAGAT
GAATTTGGTCAGAACAATTAAATCACTAAACATCATGGGGTGTGTTTTGTGTGTCTAAGT
AGCCCAGACTGGATTAAGCTTTCTCTCTTAATTTATAGCAAGTGACACAGTATTTTAAAG

SEQ ID NO: 11

10280 ATAAGAGTGCAACATAGCTACAGGGGTATAAAATTTATAATTCATGGTCCAAATGTACA
TTTGTAGTATTGATTTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGT
ATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCAGGTAAAAGGCAGCA
TTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAAT
CTTGGATTTGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGG
[A,G]

TCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTC
GTGCCCCATCCTTAGCTTTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTA
TCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCA
TGCTTTCGCCTTTGGATTCCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCC
CTTCAATTCTAAGTGCTGATGTGAATATCATGCAATATGATGTACATATTCCCATGTGC

SEQ ID NO: 12

10297 CTACAGGGGTATAAAATTTATAATTCATGGTCCAAATGTACATTTGTAGTATTGATTC
ATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGTATTTTTTAAAAATAAAC
AAAGATAAAGATTTTTTTTCTGAATTCAGGTAAAAGGCAGCATTGCTCCTCCATTTATT
ACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAATCTTGGATTTGAAAAAT
ACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAAT
[G,A]

ACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAGCT
TTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTATCTTACAAAGTACTTCG
TAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGGAT
TCCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTGCT
GATGTGAATATCATGCAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTAG

SEQ ID NO: 13

10331 AAATGTACATTTGTAGTATTGATTTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGG
GGAAAGTGTATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCAGGTAA
AAGGCAGCATTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGT
GCTCCAAATCTTGGATTTGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATG
CATGTGGGGATCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAA
[G,A]

GGAATTTTCGTGCCCCATCCTTAGCTTTCTGCTTTCTCTATTATATATGCAACTGCCT
GCCCTCTATCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCT
CAGACTGCATGCTTTCGCCTTTGGATTCCTAGATTTTCAATTAAGGTTTAGTCAGGCTAT
TGAATAGCCCTTCAATTCTAAGTGCTGATGTGAATATCATGCAATATGATGTACATATT
CCCATGTGCTGAGTAAGTAGATGTAGCATTGTCTAATGTTGCTATACATTTAGCATCTAA

SEQ ID NO: 14

10536 TACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAA
TGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAG
CTTTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTATCTTACAAAGTACTT
CGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGG
ATTCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTG
[T,C]

TGATGTGAATATCATGCAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTA
GCATTTGCTAATGTTGCTATACATTTAGCATCTAAGTTATGAACCAGATTCTACCACTGG

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FIGURE 3P



GTAACATTAATAAAAAAGTTAGGGACTTCAGGTATGTAAATATAGCAAATTCATTTCTA
CGACTTTAAAGGGTATGTGTAGAGTTCTGAAAAGAATTTCTCAGCCTCCCCCAAATCCAC
ATACTTTTGAAAGCTGATGATTGAAAAGATTAATGTGATCCTTTATTGTAACATCTAAC
SEQ ID NO: 15

11548 ACCATTGATTCTTGTTTGGAGAACATTTTGATATATTGCTTATTGGTTTTTGAGGTTGCA
TCTTTTGGGCTTATAATTTCTATATGATGTTTATTTACATGTTTGAGACTCCAGCATGGA
ATTATATGACAAAAATATTTTAGTCATTAACAATCTCTTAACAAGGCTATTTTATCT
TTGATTGTAGGGTCTTTGATTTATGAAAAATTAGGAGAAAAGGCATTTGGATGGCCGGGA
AAAATTGGAGCTTTTGTTTCCATTACAATGCAGAACATTGGAGGTAAGGGGATATACTTT
[T,C]
CAATGGATCCCATAACTTTCTATAGCGTGTTCAATAAATAAGAAAACTTATGGCAATAA
ACAGGCACCTTTAGATACAGAAAAATTGCTACTTATAGTTCTTAAATTTTAAATGATAGT
TTCTTAAATAGGTTTGTGCTGCTTTAATTAACACAGCAATATCTAAGAATGAAATAA
CATATAAACCCCTGCCAATTGAATTCTAGAATTAATAATAAAATGCTTTCTTGAT
TTTTAATGTTATTATAGCATGAATTATTACTCTTAAAAATTGAAGAATTTGTGCTTATAT
SEQ ID NO: 16

11917 TTTAGATACAGAAAAATTGCTACTTATAGTTCTTAAATTTTAAATGATAGTTTCTTAA
TAGGTTTGTGCTGCTTTAATTAACACAGCAATATCTAAGAATGAAATAACATATAAA
ACCCTGCCAATTGAATTCTAGAATTAATAATAAAATGCTTTCTTGATTTTAAATG
TTATTATAGCATGAATTATTACTCTTAAAAATTGAAGAATTTGTGCTTATATCTGTCATT
GACAAAACAGTTGACGTTTCTATGTGTGACTGAGTTGATTTACTAACTGAAAAGTGG
[G,T]
TGTCTGGGGGAACATAGCCAAATGCTGTGGTCCTTGAAACGCAGCCTGCACTGAGCCAGC
CCACTAGACAGTGTCTCTGGAAGTTTACTAAGGCAAAAGTCTGGCTAGGCATCAAATGCA
CTATAAACCCCGGTTTGTGATTCTATGGATTCTTATAATTCCTGCAATTATCATTTT
CAGTGTAGGACCTAGAAATATATATATATATTTTAAACAATGTTCTCTCGTTGGTGTGTT
TGCCACCAGCTTCATACTGTTTCTGTTGTGCTTTGGCCCTCAGAAGGCATCCAAACCC
SEQ ID NO: 17

12840 GACTATTGCAGTAGTCTTCTAACTGGTCTTCTGGCTTGAGTTTCCCCTGCTCTCAGATA
AACTCTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTG
TGCATAAAATTTCTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAACTCATTGGAC
TGACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCTAGCAATGCC
CATATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT
[T,-]
ATCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAA
TTATATTTATTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTT
TTCACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCTCCAACCCTAACACACACG
CACACACACACACACACACACACACACACACACATTTTCTCTCACTCTGCTCAC
CTGGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTTCTCTGGGCTCTCATGGTCTGT
SEQ ID NO: 18

12844 ATTGCAGTAGTCTTCTAACTGGTCTTCTGGCTTGAGTTTCCCCTGCTCTCAGATAAACT
CTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTGCGCA
TAAATTTCTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAACTCATTGGACTGAC
ACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCTAGCAATGCCATA
TCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC
[A,-]
TCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAATTAT
ATTTATTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTTTTCA
CAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCTCCAACCCTAACACACACGCACA
CACACACACACACACACACACACACACACACATTTTCTCTCACTCTGCTCACCTGG
TCTATTGCTCCTCTAGACTGGTAAATACTAGTTTCTCTGGGCTCTCATGGTCTGTTTGT
SEQ ID NO: 19

12847 GCAGTAGTCTTCTAACTGGTCTTCTGGCTTGAGTTTCCCCTGCTCTCAGATAAACTCTA
ATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTGCGTCATAA

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FIGURE 3Q



AATTCTTCAGCATGCCTTTATTATTTTCAAGGAAAACTTAAACTCATTGGACTGACACA
AGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCTAGCAATGCCCATATCT
ATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC
[T, -]

ATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAATTATATT
TATTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTTTTCACAG
GCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCTCCAACCCTAACACACACGCACACAC
ACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCTGGTCT
ATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGTTTGTATC

SEQ ID NO: 20

13019

CTGACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCTAGCAATGC
CCATATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT
CTATCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACA
AATTATATTTATTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTC
TTTTACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCTCCAACCCTAACACACA
[C, -]

GCACACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCA
CCTGGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGT
TTTGTATCTAGTATGTTACTGTTTTCTAAAGGATATTTTAAAAACTTGAGTAGAGAATA
AGCTTTTGGAGTCTGATGGACCTGAATTTGAGTCTGTTTCTGTCACTATCTGTGAACCTG
GGAAGATCACTGTACTCCTTTGTCTGATTTTTTTCATGTATAAAAAATTACCTTACAAAGGC

SEQ ID NO: 21

13022

ACACAAGATCTTCGTCTAGTTCTTCTGCTCAATCTTTCTAAACTTTCTAGCAATGCCCA
TATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTA
TCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAAT
TATATTTATTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTTT
TCACAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCTCCAACCCTAACACACACGC
[A, G]

CACACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCT
GGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGTTT
GTATCTAGTATGTTACTGTTTTCTAAAGGATATTTTAAAAACTTGAGTAGAGAATAAGC
TTTTGGAGTCTGATGGACCTGAATTTGAGTCTGTTTCTGTCACTATCTGTGAACCTGGGA
AGATCACTGTACTCCTTTGTCTGATTTTTTTCATGTATAAAAAATTACCTTACAAAGGCAT

SEQ ID NO: 22

13285

ACTGTCTCTCAAAGTCTCCAACCCTAACACACACGCACACACACACACACACACACACA
CACACACACACACATTTTCTCTCTCACTCTGCTCACCTGGTCTATTGCTCCTCTAGACTG
GTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGTTTGTATCTAGTATGTTACTGTTTT
CTAAAGGATATTTTAAAAACTTGAGTAGAGAATAAGCTTTTGGAGTCTGATGGACCTGA
ATTTGAGTCTGTTTCTGTCACTATCTGTGAACCTGGGAAGATCACTGTACTCCTTTGTCT
[G, A]

ATTTTTTCATGTATAAAAAATTACCTTACAAAGGCTATTGTGAGGATGAAATAAGGTAACA
TATGGCACATAATAAGTGTTCTGTATATGCTTCTCTCCTCCCTGGTCTCTGCTTCCATA
TCCATGTCTCTGGAGTTGCCTGAATTTATTTTAAATAGGCATTTAAAAAATTATAAAAC
AAATATATGATGATTGTGAAAAACTAAAACTGCATAAATATATAAATTACCAAGAAAA
GTTTATGTGAGTATCCTCAGAAATAACTACTCATAGGTTTTCCCCTATGCCTAATTCAA

SEQ ID NO: 23

14461

TATCGAGCATTTTCATAGGATTGCCTTATAGTTGGTCTAATTTAACAACCTGAAATAACCAG
GCATAAGCATAATTAACCCTGGACTCAAGAAGTTGAGTGGCAGCACCTCAGCTGTGGTTC
AAAGCATAGCCACTACTACGCTTCTAAACAATGGAATAAAGTATAAAGCGGTCTCTCAGT
CAAGCCTCACACAGGTAAGAGGCGTGACTTTAAGGGAGTAAGATGAAATATCGTAACATC
ACCCGAGAAATAATGCTCTCACTTTGGTTACTTTATTTGATTAGTTGATATTTGGCATAA
[G, C]

AGAAATCACTTGATTTTCTCTATTTAACAACCTCTACATTTAGAACACTTAATTTTCTCAA
TCCCCTAAAAAATTAACATTTACTGCAGATGTTTTACATTAACAGATTAATGTCTGGAT

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FIGURE 3R



15464

CATTCTGAATTTTTGAAGACCAACATGTTAACATCACTGACATCACTGAAAACCAGCAA
TTAATAGCTGTAACATTGAATGGTACCTACCAAGCCAGCTAATCAGAAATATCTCCTGT
GTTCACTCTGTAAGATTTAGCTTTAGCCAAGGTCTTTGCAAAGATTAACCAAATAATG
SEQ ID NO: 24

TGAGTTCTATTTTTAACTGAATCTTTTGCCCATGTGTCAACAAATTAACGTTATCCTTCA
CCAAATGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATT
GTAATGTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGATGATTTTCAT
CAAGAAATCTTTCACAAGAGTAGATAATCATTATGTATCACTTACCTAGATGCTCATGA
AATTTTGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGG
[-,G]

AAAAAAAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATC
AATCCAGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTAATCCTCAGAT
AGGTCCCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTC
TGCAGATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGAC
TACTGCCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATA

SEQ ID NO: 25

15469

TCTATTTTTAACTGAATCTTTTGCCCATGTGTCAACAAATTAACGTTATCCTTCACCAA
TGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAAT
GTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGATGATTTTCATCAAGA
AATCTTTCACAAGAGTAGATAATCATTATGTATCACTTACCTAGATGCTCATGAAATTT
TGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAA
[-,A]

AAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATCAATCC
AGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTAATCCTCAGATAGGTC
CCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAG
ATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGACTACTG
CCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAA

SEQ ID NO: 26

15545

AGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAATGTTATGTATATGAATA
CATATTCATTTTTTCAGGGAGAAGGCTTGATGATTTTCATCAAGAAATCTTTCACAAGAGT
AGATAATCATTATGTATCACTTACCTAGATGCTCATGAAATTTTGCCACTTTATATAAT
TCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAAAAAAAACTTCTTTGAC
AAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATCAATCCAGGAAGCCTTTGGTT
[T,C]

TGACAATAAGTGGTCTGAGACTTTGTGTAATCCTCAGATAGGTCCCGGAGGACTAGATTG
GTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAGATCTGCCCTTTGATTC
TGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGACTACTGCCCAAGTTATAGACAC
TAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAATGAGGGCAGAACCTTA
GAAGTGCAGCTTCACTGTAACTTTGGAGCAGGATTTAACACAGAATCAGCCCTGATACT

SEQ ID NO: 27

16199

AGAACTTGGAAGCAGTGCCAAATACACAATGACTTTTTTTCCATTTGGGGGATTAGATG
TTCATCTTACATATCCCAAATGTCATAACTTGCTTGATGTGACTTCAGTACTGTCCACA
CCATTAAGCTGTCACATTTCCATTTTAGCAATGTCAAGCTACCTCTTTATCATTAATA
TGAAGTACCTGAAGTAATCAGAGCATTATGGGACTTGAAGAAAATACTGGGTATGTCTT
ATGCTCCCTCTGTGACATCAAGTGAATCTTACTTGGTCTTTCTGATTCTAATATCC
[T,C]

TGTCTCTCACTTCTAGAGAATGGTACCTCAATGGCAACTACCTCATCATATTTGTGTCTG
TTGGAATTATCTTCCACTTTTCGCTCCTTAAAAATTTAGGTAAAGATATTTCTAACTGG
AAATATTTTTATTTTTATTTACATTTAAATAGGTTAGCTAATTGTAGATGCCATATTCA
CCTTCCAAAATGCTTCTTCTAACTTCTAGGTTATCTTGGCTATACCAAGTGGATTTTCTCT
TACCTGCATGGTGTTTTTGTAGTGTGGTAAGTGATGTGATGACATGATCCTTGACAGGT

SEQ ID NO: 28

16798

GTTGGTTAGCATGAGTTTTTTTTGTGCCTAAATTAGTGTCTCATTTTGTTCAGCACTTC
ACTAATATGAAATAGTTCTTGATCACAAGTGATTTCTTGAGACTAATTTAGAGCAAA

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FIGURE 3S



AAAAGAGCAGCTACGATTTAAAGATAGTTGAGGTAGAATATCAAAGCTACTACTAATGCT
TTGGTCTAGGCACACTGGTTATATATGGGGAAAAAAGGAAACTTCAAGCAGGAACATGA
CAATAATCTGGCATTTAGAACAGCAGAGGAGAGTCCCAGATGAGAAACAAGAAGGCTATA
[T,C]

CCATATTCACATGAATCAGCCATTCTCTCTTACACATTCCACCCATTAAGAGAGGACAAG
AACAGTGGGATTAAAGAAGAAATCCTCCTCTAGGCCCTGACAAAAGAGGGAATTTCT
TGCATATCATGAATGCCAAAATTTATAAAGCATTTCCTCAAGAGGTAAAGGAGAAGGA
AAAAAAGTTTTGAAGACCCATGTCACCTTAGTTTGAAGAAATAAGGAAATGATCATCTTT
CTCATGGAAGGGCATGAAAGAGGGTGGGAAGGATTCTTGCAAAATATTGCTCTGTTAACT

SEQ ID NO: 29

18103 CATTTTAGCATTCTAATTTGCTTTGAAATTCTGCTCATATGTTCAAAGATTCTTTAACAG
GAAACACAGTTTATAGCTTCTCTTTCAGAGAAAATATGTACTCCATCCACTCCTCAGTAA
CATGCTTTAATCAGAAAGTGGGAATCAGCCCACCACAGCACTACCTTATCTTCTTCTC
TCCTTTCTCTCCACCATAATGGTTTCAGGGGAGGGGTTTCATGGCAGGTGGACAAGGAGTCG
ATGGTTGTAATAATTTTGGCAGGTGTTGGGAATTTAAATTTGAATTTTGTTCGGAAGAAA
[C,T]

GATGTCAGCTGGACTAGAAATGAAAACACCCATGACGACCAAACTTATGGTTAGGGGCA
GCCTCGATAAGCCAGTGATGTCATTTATAGTCAGCACCTAACCTTGTCTAGAACACATT
CATTACAAGAGATGTGTCAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACT
GGCTAGAAAATCTTGTTCTTCCAGCTGATGGTCTATGGTTCAATTTGATTCTTTTCCCT
TTGAAGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACCTATTATAGCTGTTTTCCT

SEQ ID NO: 30

18421 AAATGAAAACACCCATGACGACCAAACTTATGGTTAGGGGAGCCTCGATAAGCCAGTG
ATGTCATTTATAGTCAGCACCTAACCTTGTCTAGAACACATTATTACAAGAGATGTGT
CAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCTAGAAAATCTTGTT
TCTTCCAGCTGATGGTCTATGGTTCAATTTGATTCTTTTCCCTTTGAAGTTGTTGATATT
TGCTTGGGAACAAAGGATATGAACCTATTATAGCTGTTTTCCTTTTCCCTTTAAGGGAGG
[A,G]

TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
CACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAAAAAATTTCAGAACA
CTTTCAAGTATTTTGATGCTTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTTCAGAAGCTTTT
CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCCTCAT

SEQ ID NO: 31

18528 ACAAGAGATGTGTCAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCT
AGAAAATCTTGTTTCTTCCAGCTGATGGTCTATGGTTCAATTTGATTCTTTTCCCTTTGA
AGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACCTATTATAGCTGTTTTCCTCTTT
CCTTTAAGGGAGGATATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACC
TCAGTCTTCATTCTCACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAA
[G,A]

AAATTTCAGAACACTTTCAAGTATTTTGATGCTTTTGATTTACTTTGAAAATTACATGTA
GCAGTTACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTT
TTCAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGG
TTCTTTTCTCATTTAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGC
CTGTTTCATCTTTATGTTAATTATATTCTTATTAGTGGGCAAGCTTACTGACCTACGTG

SEQ ID NO: 32

18722 TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
CACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAAAAAATTTCAGAACA
CTTTCAAGTATTTTGATGCTTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTTCAGAAGCTTTT
CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCCTCAT
[T,C]

TAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCTGTTTCATCTTTA
TGTTAATTATATTCTTATTAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCC

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FIGURE 3T



TCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAAT
GAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATA
GTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGA

SEQ ID NO: 33

18775 TCATTCTCACTAAATAGCAAACTTTCCCATAAATTCTGATTTACCTCATAAAAAATTT
CAGAACACTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTAGCAGTT
ACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTCAGA
AGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTT
TCCTCATTTAAAGTCATCTCATTATGAAATGCAAAGCTTCTATGTTAGGAGCCTGTTT
[C,G]

ATCTTTATGTTAATTATATTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGA
CTGTTCTCTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAA
TGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTAC
TAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGA
AAAGTGATTTTTTTTTGTAAGTTTAAAAACAAAGCTTGGTGTCTTTCTTTTCCAGTC

SEQ ID NO: 34

18951 CAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTT
CTTTTCTCATTTAAAGTCATCTCATTATGAAATGCAAAGCTTCTATGTTAGGAGCCT
GTTTCATCTTTATGTTAATTATATTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAA
ATAGACTGTTCTCTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAG
AAAAATGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTA
[T,C]

GTACTAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATT
TTGAAAAGTGATTTTTTTTTGTAAGTTTAAAAACAAAGCTTGGTGTCTTTCTTTTCC
AGTCGGTCCCGAGAAAAATGCAAACGGTGTCAAATATTTCCATCACGGGGATGCTTGTC
ATGTACCTGCTTGCCGCCCTCTTGGTTACCTAACCTTCTATGGTAGGTCCTCTGAAAG
TCATTCTCTATATGCAAATCCTTGTTAGGCTGGTCTTGACCTGGGTAGGTATGATTTTT

SEQ ID NO: 35

18974 ACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCTCATTTAAAGTCATCT
CATTATGAAATGCAAAGCTTCTATGTTAGGAGCCTGTTTCATCTTTATGTTAATTATA
TTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCTCTCTAGGGA
AATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAATGAATCCTCATT
AGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATATGTCTTCATGAT
[T,G]

AGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGATTTTTTTTTGTA
AGTTTAAAAACAAAGCTTGGTGTCTTTCTTTTCCAGTCGGTCCCGAGAAAAATGCA
AACGGTGTCAAATATTTCCATCACGGGGATGCTTGTCATGTACCTGCTTGCCGCCCTCTT
TGGTTACCTAACCTTCTATGGTAGGTCCTCTGAAAGTCATTCTCTATATGCAAATCCTT
GTTAGGCTGGTCTTGACCTGGGTAGGTATGATTTTTTAAAAATTGCCTTCTATAAGCATG

SEQ ID NO: 36

19540 GGTATGATTTTTAAAAATTGCCTTCTATAAGCATGCTCTATAGATGACACATATTCAATT
AATACTATTTTAGTTTTGTCACTTGACCTGAGGAAATGGGGCCTGATTCAGCCTGGCT
AACAAGTTACAAGAATTTGTGAATTAACACCTATTTTATAAAAAATATCCCTCAAACAAA
ATTATTTTCTCTAGGGATAGATGATTTTCTCTGGCTAGACTCCATAGTCCAACCTCAGG
CTACAAGTGATGAGAATGAATCCACTTGATGTGATAAAGCTCCTTTGATGGAATTATTA
[A,C]

CTGCCACACAAATAGCAGGGAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTCT
TATTTTGTATACTAAATGATTTCTAAGAAAGAGGACATGACAGAATTTCTTCAATCT
AAGAATGCACCACCAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTCT
CTCTCTGGCATCTTAACAGTTCACAAAGGAGTAGGATTGTACTCCTTCCATGAAGTGTG

SEQ ID NO: 37

19841 CTGCCACACAAATAGCAGGGAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTCT

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FIGURE 3U



TATTTTGTATACTAAATGATTTTCTAAGAAAGAGGACATGACAGAATTTCTTCAATCT
AAGAATGCACCACCAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTCT
CTCTCTGGCATCTTAACAGTTCACAAAGGGAGTAGGATTGTACTCCTTCCATGAAGTGTG
[G,A]

CCACATAACAGATTTTCATGGAATCACATATTGACCTGGTAGCATATGTTTACATGAATC
AGTGTATCAATATAAATATATTTTTGTATAAACCTCCTTTTAAAGTTTTTAACTTAATTT
TTTTCTTACTGACTTGGTAAATTGAATTGCATGTATGACAAATTGTGGAGGAAAAGATTCT
AGGAGTAGGCCACCATTGTCTTAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAAC
CAACATGTGCTTTAGATTGGGCATTAACTTTTTGCCGGTTGTGAAATAATGAATGACGA

SEQ ID NO: 38

20170 TATTGACCTGGTAGCATATGTTTACATGAATCAGTGTATCAATATAAATATATTTTTGT
TAAACCTCCTTTTAAAGTTTTTAACTTAATTTTTTCTTACTGACTTGGTAAATTGAATT
GCATGTATGACAAATTGTGGAGGAAAAGATTGAGGAGTAGGCCACCATTGTCTTAGGTTT
TTTTCTATTTGACTAATATTTGACTATTAACCAACATGTGCTTTAGATTGGGCATTA
CTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTATTTTCACT
[A,C]

CTTTTTGTCTGATCTTGAGGTGAAAATCCAACCTACGCTTGATTCCATAGATATTTTCTTG
TTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCTTCGTCTTA
GAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCCTGCAGTTACTT
ATACTTATTTTAAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCCAAAAATATCT
GTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGTAGCAATCATTCA

SEQ ID NO: 39

20343 TAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAACCAACATGTGCTTTAGATTGG
GCATTAACCTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTAT
TTTCACTACTTTTTGTCTGATCTTGAGGTGAAAATCCAACCTACGCTTGATTCCATAGATA
TTTTCTTGTTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCT
TCGTCTTAGAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCCTGCA
[T,C]

GTTACTTATACTTATTTTAAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCCAAA
AATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGTAGCAA
TCATTATCTAGAGTTTACACACTGGGTTTGTAACTGCATCAGGAGTGGCTGCACAGG
TAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTCATCC
CCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGGAGAT

SEQ ID NO: 40

20519 GATATTTTCTTGTTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGC
ATCTTCGTCTTAGAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCC
TGCACGTTACTTATACTTATTTTAAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGC
CCAAAAATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGT
AGCAATCATTATCTAGAGTTTACACACTGGGTTTGTAACTGCATCAGGAGTGGCTGC
[G,A]

CAGGTAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTC
ATCCCCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGG
AGATAGATTTATCACAATGTAATGAGCTTGAGAGGCTCTTTATTTTGTATTATACCTTC
TGCAACGTTATCAGCTTCAGGACCTCTTTGTTCAATTTGAATGAAGGTTGCATAGCTAATG
AGCTCAGAGGCAAGACCAGAGGTGCCTGGATTCCAGGCCTAGGCTTTTCTCTGTTCT

SEQ ID NO: 41

20963 TGAGCTTGAGAGGCTCTTTATTTTGTATTATACCTTCTGCAACGTTATCAGCTTCAGGAC
CTCTTTGTTCAATTTGAATGAAGGTTGCATAGCTAATGAGCTCAGAGGCAAGACCAGAGGT
GCCTGGATTCCAGGCCTAGGCTTTTTCTCTGTTCTGTGTTCTCTCTATAAAATGTTGC
CATAAGTGACCTGTGCTGATTTGACAACACCAAGCGGTTTCATTCTCTTTTCTGTTGT
AGGAGAAGTTGAAGATGAATTACTTCATGCCTACAGCAAAGTGTATACATTAGACATCCC
[T,C]

CTTCTCATGGTTGCGCTGGCAGTCTTGTGGCAGTAACCTAAGTGTGCCCATTTGTCCTC
TTCCAGTAAGTACATAAGACTTTGATGAAAGAAACCTACTTGACCCCATAAATTAGTAC

FIGURE 3V



ATGTGTTCTACCTTCATTTTGATTTAATTATAGGGTGAGTTTGCAATTGCAATGCCTGAG
GATATTATTTTCTATAGCATTTTGAGTCACTTAAAATTGGCCATTTAATGTGTAGATAG
AGCAAGTAGTTTCAGGTGGTATTTTATAGTGTAGGAAAAAATCATAAAACCTATTTTT

SEQ ID NO: 42

21840 AAACAGTTATGCTATCTATCACATATCTCTCACACATGGCCTCTGCCAGACTCACACC
AGGTCACCCCTCCCTGGCATTTGTCTTGGTGTGAGTTTGTCTGAGATCCCAGAGCAGA
GCTGGTAGTGAAGATTTGGGCTGTGTGAGTTAAAACCACCACCTAAGGATAAACACAGGT
CTTCAACCCTCCTGCCAGCTCCTGTTTCATAAACACTGAATTTACTCATTCAATTTGAGGGG
GAAAAAATAAGTGACACAGTAACCAGCACTGTCCTGGACATAATGTTCCATACAGGGCT
[G,T]

GCATATGAAGACTATTTCTATAATGACACTGTGGTCACTTTAAATGCAGCTTGTGTGCTG
AAATATATTTTGGCACATTCCTTTTTCATGAGTGCATGAAATCAGATCCGTAATACTATG
GTGGCTAATATTTTACTCTTAAATCATGTCTTGCCTCTAATATATCTGAAAGTATTTTCA
ATGACATACACATAGCTTTAGCCTAAAATCAGTCCGTCTTGGGTACAAGACAGAAGACA
ACTATAAACAGAAGGTATACGATAGGGTAAAATTGCCAGGCAACAACCTTCACTGAGAAA

SEQ ID NO: 43

22783 TGAGAAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAACATT
AGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTGAGAAAAATGACTAAGTGC
TGTCTTTCATTATGATTTTCACTCAACATTAGCATTTATGAAACATTTTGCACATTATC
CTGTCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCAC
AGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTC
[C,T]

GTCTGTCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAA
ACTGCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTC
AGCTGGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTATACATGAAGGATACACAG
AGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCTCTGAAGCTA
AATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTT

SEQ ID NO: 44

22787 AAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAACATTAGAT
GCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTGAGAAAAATGACTAAGTGTCTGTC
CTTCATTATGATTTTCACTCAACATTAGCATTTATGAAACATTTTGCACATTATCCTGT
CCTCACCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC
[G,A]

TGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAAACTG
CCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTCAGCT
GGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTATACATGAAGGATACACAGAGAT
GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCTCTGAAGCTAAATT
CAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT

SEQ ID NO: 45

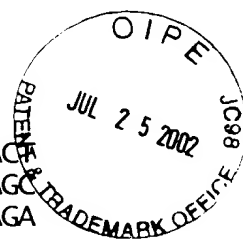
22825 CAATAGTGTGTAACATTAGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTC
AGAAAAATGACTAAGTGTCTTTCATTATGATTTTCACTCAACATTAGCATTTATGA
AACATTTTGCACATTATCCTGTCCTCACCCTTGCAATGTTACATTTATATAATCTGTGTA
AGTGCTCCACTGCCCCACAGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACT
GGCACAGAGGGTGAGCTCTGTCGTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGC
[T,C]

TTGTCTTGAAATGTATAAACTGCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGT
GACATGTGCTACGAATTCAGCTGGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTA
TACATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAA
TCAAGTCTCTGAAGCTAAATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTAT
TGGCGCTTTTGCTTGTTTATTTTCGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATG

SEQ ID NO: 46

22967 CCTCACCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC

FIGURE 3W



GTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAAACT
GCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTCAGC
TGGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTATACATGAAGGATACACAGAGA
[A,T]

GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCCTCTGAAGCTAAATT
CAATTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT
CGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCTGACTCACAGCATGGTTCTCC
TGACAGTTTATTTTATTTAAGGAACTCTTACCAGTAAGTTTATTTACTTGCCTTGATAT
CTCCACACATTAATAATAAACTAACAAAACCTAATCTGAATTAAAATCTATCAGCTTTA

SEQ ID NO: 47

23248

CATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATC
AAGTCCTCTGAAGCTAAATTCAATTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTG
GCGCTTTTGCTTGTTTATTTCTGATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCT
GACTCACAGCATGGTTCTCCTGACAGTTTATTTTATTTAAGGAACTCTTACCAGTAAGT
TTATTTACTTGCCTTGATATCTCCACACATTAATAATAAACTAACAAAACCTAATCTGA
[A,G]

TTAAAATCTATCAGCTTTAGGCATTATTTTGTGTTCTCCTTCTTTCAACATGGTAACTGG
GCTCTCTTTCTTAGGAGCTTGAGAAGATATGACTGGGGTTTGTCTTCTACTTCATTT
ATTATCTTTCTTTTCCAATCAGTTAGTTTTTCTTTTGTAGTAAAGGTGCATAGTA
ACTGCTTGTAGTATTTGTTGAACAAGTGAATAAATGAAATGAATTAAGGTAGTGTTC
CTAGCAGCCCAACATTTCTTTCTCTTAGTAGTGGGTGGGTATCAGTTATGGAATGGC

SEQ ID NO: 48

23764

GAAATGAATTAAGGTAGTGTCTTCACTAGCAGCCCAACATTTCTTCTCTTAGTAGTG
GGTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCAATTTTCAG
CTTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAAT
AATCCTAATGGATATATAATGAACACACAGATGAAAATTTACCTGCCATGCCTTTGAAA
AAAGATCCCTAGCTACTTGTATTTTATCTTATAATTAATAATCAGTCTTTTCACTTATGTT
[G,T]

TCTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATT
GCTATCAACTGCAGTGGAGCAGTGATTCTGAGTTTTCCAACATCCTTGCCTTAAGCAAA
CCTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTT
AAGAGTTAGAATAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTGACCTTCACATT
GGGCCCCCTGCATCAGAATACAGCACCCCTAACAGGCTCCTGTTCAGGACTCTTCTCTG

SEQ ID NO: 49

23765

AAATGAATTAAGGTAGTGTCTTCACTAGCAGCCCAACATTTCTTCTCTTAGTAGTG
GTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCAATTTTCAGC
TTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAATA
ATCCTAATGGATATATAATGAACACACAGATGAAAATTTACCTGCCATGCCTTTGAAA
AAGATCCCTAGCTACTTGTATTTTATCTTATAATTAATAATCAGTCTTTTCACTTATGTT
[C,T]

CTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATTG
CTATCAACTGCAGTGGAGCAGTGATTCTGAGTTTTCCAACATCCTTGCCTTAAGCAAAAC
CTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTT
AGAGTTAGAATAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTGACCTTCACATTG
GGCCCCCTGCATCAGAATACAGCACCCCTAACAGGCTCCTGTTCAGGACTCTTCTCTGG

SEQ ID NO: 50

24432

GGATGGTGCTGGGGACCTCCCTGACCCACAGCATCTGACCCACATTTCCAGGTTCTAGC
GACTTGTGTGAGTAAAGAAAAAGGCACATAGCTAAGTGGAAGAGCAGATGAGGCTTGGTG
GGAATCAGCCAGTGGTCTGCCCTAGCAAAGTAAACAGAAGTCTGGGGGCTTTTGGTCC
TAGGCTCACTACTCAGGGAGGCACTTTAATGGAATGACCAGCAAGTTTCTTCTCTGAT
CTTTTCCACCACCACCAAGCCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTC
[A,G]

GGAATGCACTGGAACCACCTTCAGTTCTGTTTGAATTTTCTATTCTTATTTCAGAAA
GAGGAAGAAGCTTTTGATTTACTCCAACCGTTCTACCTATTATTCCCATAACTTTCTG

FIGURE 3X



TGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTTACAC
TTCAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTT
GAATGCACCTTTTTTAACAAGTGAATAAAAAACAACTGTGACTATTCTCTGAAAATGAGC

SEQ ID NO: 51

24538

GATGAGGCTTGGTGGGAATCAGCCAGTGGTCTGCCCTAGCAAAGGTAAACAGAACTGCTG
GGGGCTTTTGGTCTAGGCTCACTACTCAGGGAGGCACTTTAACATGGAATGACCAGCAA
GTTTCCTTCTGATCTTTTCCACCACCACCAAGCCTAGTACCTCCCTCCCTCTTTGCT
CTGTTGCTCTCTTCGGGAATGCACTGGAAACACCTTCAGTTCTGTTTGGAAATTTCTTA
TTCCTTATTCAGAAAGAGGAAGAAGCTTTTGCATTTACTCCAACCGTTCTACCTATTATT
[C,G]

CCATAAACTTTCTGTGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGG
AGACTGCTTTTACATTTCAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACT
CAGCTTATTGACTTGAATGCACCTTTTTTAACAAGTGAATAAAAAACAACTGTGACTATT
CTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGTTTAACTGTGAAAACAAATT
AAGTCTCTGGCACTATGTATATACCATAAAAAGCTTATTTGTAAGCCTACTAATTGGAC

SEQ ID NO: 52

24693

CCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTCGGGAATGCACTGGAAACCACC
TTCAGTTCTGTTTGGAAATTTTCTATTCTTATTTCAGAAAGAGGAAGAAGCTTTTGCATT
TACTCCAACCGTTCTACCTATTATTCCATAAACTTTCTGTGATCTCATATCATTAGGCC
AAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTTACATTTCAGAGGCCCTGGACATAT
AGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTTAACAAG
[T,C]

GACTAAAAAACAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTAT
TCTGTTTAACTGTGAAAACAAATTAAGTCTCTGGCACTATGTATATACCATAAAAAGC
TTATTTGTAAGCCTACTAATTGGACCAGTTTGGACAATATTGAATAAGCACTAATTGCAG
ATCATAATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTCCTTTCCTCA
GTTTCCTTTTTCAGAAATGAGTTTCATAATGTTCACTAATCCAATTTTTTAAATCCTTTACA

SEQ ID NO: 53

24819

AACCGTTCTACCTATTATTCCCATAACTTTCTGTGATCTCATATCATTAGGCCAAATGT
TAATCTTTCTGGGAGCCAGGAGACTGCTTTTACATTTCAGAGGCCCTGGACATATAGGACT
GCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTTAACAAGTGAATA
AAAAACAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGT
TTAACTGTGAAAACAAATTAAGTCTCTGGCACTATGTATATACCATAAAAAGCTTATT
[C,T]

GTAAGCCTACTAATTGGACCAGTTTGGACAATATTGAATAAGCACTAATTGCAGATCATA
ATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTCCTTTCCTCAGTTTCC
TTTTTCAGAAATGAGTTTCATAATGTTCACTAATCCAATTTTTTAAATCCTTTACAAAGTTA
TTCTTAACTATTTCCAGAGACTATCTGGTTTGTCTATTCTAGAAATGAAATTCCTTTTC
AGCCTAAACAGATGGCCTTAATTTTTTGGTGGAGTGGTATGAAAGGAATGTCACATGAGAA

SEQ ID NO: 54

25743

TATCCAGTTACAGCAGCGTAACTTGAGCAGCTGCTGCAAACCTGAGGCTCTCTTGACCCCT
CGCCTACTTATTTTCACTGCTAAAATAGGGCTGAAATCTGTCAAGGATCCTGAAGGGAAG
GATAAGATTCCTACTATTCAATTTAATTTAAGCTTTTATTTCAGTGCCTGCTGTGTGCACA
ACACTAAGCTAGAAAGTCTGAGGAATGTTTAGATTATTAGGTCTGTTCTTGCCTTTTCA
TAGATTTACAATCTATTGATAGGGAGAGCTAAAAAGGAGAGAAAGAGGAAGGAGCAAACA
[C,T]

AAAAACGTCAAAATTTTTAAATACCATTTTTAAATTTTTATTTTAAATGTTAAATACCAT
GCAAAATTAAGGAAAACCTAGATTTCATAAAAATTCCTTTTCAATCTTGTGTAAATCAAT
TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
GTTTTACTATGTTTCTTAATTTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
TTTAAACAATAAATCTGAAAACCTAAGAAAGTGAAGCATAAAATATTGCTTATATAAAATA

SEQ ID NO: 55

26044

AAAAACGTCAAAATTTTTAAATACCATTTTTAAATTTTTATTTTAAATGTTAAATACCAT
GCAAAATTAAGGAAAACCTAGATTTCATAAAAATTCCTTTTCAATCTTGTGTAAATCAAT

FIGURE 3Y



TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
GTTTTACTATGTTTCTTAATTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
TTTAACAATAAATTCTGAAAACCTAAGAAAGTGAAAGCATAAAATATTGTCTTATAAAAATA
[G,C]

GCCAAGGAAAAAATGACACTCCATTTCAAATATCAAAAGTTAGCATCAAGACTGCACAAG
ATGAATGTACAGTCATGTGTTGCTTACAAATGTGGACATATTCTGAGAAATGCATCTTTA
GGCAATTTTGTCAATTGTGCAAAACCCATAGATTGTACTTGCAGCCTAATTGGTGGAGCCT
ACTATACACTAAGGCTATATGGCATAGCCTAGTACTCCTAGGCTACAAACCTGTACAGCA
TGTTACTGTACTGAATAGTGGAGGTACCTGTAACATAATGGTAAGTATTTGTGTCTCCAA

SEQ ID NO: 56

26555 AGTACTCCTAGGCTACAAACCTGTACAGCATGTTACTGTACTGAATAGTGGAGGTACCTG
TAACATAATGGTAAGTATTTGTGTCTCCAAACGTAGAAAAGCTACTGTAAAAATACAGTA
TTACAACCTTAGGGTATCACTGTCTTATATGTGGTCTGTTGTTGACCGAAATGACTATGC
TTAATACCACTGAAGTGTACACTTAAAAATGGTTAAGATGGTAAATTCTATGTTATGTAT
GTTTTATAATAATAAAAAAATTGAAAAAAGCATCAACATCTTTCTGGGAAAAAAGAAAA
[G,A]

GAAAGAAAATGCATTAGAGTGATGAGAATATTTGAAGTAATAGATAAAGTCAAAAAACAA
GAAATGATCTTGCCTTTGAACCTTCTGTTAAGATTCGTACATCAGTGATCACACTGTT
ATTTCCCAAACGACCCTTCAGCTGGATACGACATTTCTGATTGCAGCTGTGCTTATTGC
ACTTAATAATGTTCTGGTCATCCTTGTGCCAACTATAAAATACATCTTCGGATTCATAGG
TGAGTTTCAGAAAGGCTTCAATTGGTCAACCCAAACTCACGCTCATTAAATGATGGAC

SEQ ID NO: 57

27886 GGTTTATTTAAAGTGTGTGCTGGCATCTCCTTTGCTAGGAACTGCTGGGTAAGACATTGA
CCTTGCCCTGTGTTTGTCTTCTCAGGGGCTTCTTCTGCCACTATGCTGATTTTTATTCTT
CCAGCAGTTTTTTATCTTAACTTGTCAAGAAAGAACTTTTAGGTACCCCCAAAAGGTC
GGGGTAAGTAAACCTTGCAATTTCCCCCATTATTAGTTGTTCTTCCACTACTTAGAATA
AACTAGAAAATACACATAGTTCAGAAAAATGAATCAATGTACAAGAACCAAAAATCAAAA
[A,C]

TGGGCTAGAACCTTCTGGTAGCAGAGAAAGGGGACATATTTCTGAAACTCAAATGATTCT
ACTTCAAATATCAAATATCCTGTGTTGAGTCTGTCATACATGTCAAATAGTAGTAGCCTT
TCCCACAGACACATATGCTTCAGGCAAATAGCAGTGTCCAATACCAAGCTGCTGTTGTGC
TATCCGTGGAAAATCATGCAAGAAGGAATTAGGCTCCCTAGCGGTGTTATGGAATAATTT
AAATATTTTGGTCATGGTTGTTAGGTTTGCAAAGCCAAAGGAAAGATGTTGCTTTTGTGTT

SEQ ID NO: 58

31884 CTTTTATGGTTAGTTTGAAAGAATCCATTGAAGATAGAAAATGAGAGAATAGAAGAAACC
TGAGAATAGTAAAATAAAGAGCAGAGAAAATATGGGGGCAGGGAAAAACATGTGAGTGCTA
AGGATTGATTATGAATGAACGATTAGGGGGATTGATGGATCACAGGGTAAGTATATGCTT
AACTTTATAAGAACTTCCACATAGTTTTCCACAGTGTCTTACCATTTTCATTTCCACC
CGTACTACCTACAACCTTCCACTGACTCCACAGCCCTGCCAACATTTGGTGTTGTCTTTTG
[T,C]

ATTTTAGCCTTTCTAGTGGGTCTGAAATGGTAACTCATTGTGATTTTCATTTCTGCTTCT
GTGACAACTAATGTTGAAAACCTTTCAAGTGTTTAAATGGTCACTCATATATCTTCTTTTG
TGAAGTGTGATTCAAATCTTTTGCCCATTTTAAATTTAGGTTATGTGTTTTATTGG
GTATTTGTAGAAGCTCTTAAATATGGATCCATGTCCAGATTGCCAATATATTTCCAG
TCTATGGTATGGTTGCTTATTTTCTAAAGGTGTCTTAATTACATCTTTCTGGGGCCAGG

SEQ ID NO: 59

32229 TTTCAATTTCTGCTTCTGTGACAACTAATGTTGAAAACCTTTCAAGTGTTTAAATGGTCACT
CATATATCTTCTTTTGTGAAGTGTGATTCAAATCTTTTGCCCATTTTAAATTTAGGT
TATGTGTTTTTATTGGGTATTTGTAGAAGCTCTTAAATATGGATCCATGTCCAGATTGC
CAATATATTTTCCAGTCTATGGTATGGTTGCTTATTTTCTAAAGGTGTCTTAATTACA
TCTTTCTGGGGCCAGGTCAACATAGCTCAAAGTTTGCAATTTATGTCTTAATGAGATAA
[T,A]

ATTAATCAGAGTGGTATAGTCAAAATTAATGTTTTGATGTCTGGGCCCATATAGGTAG
GACTGGATCATCTAACCAAGATGCAAAAAAAAAAAAAACAAAAAATAGTACTTG

FIGURE 3Z

Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



GAAAACTTATTTTAAATTAAACA

SEQ ID NO: 60

FIGURE 3AA